GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2005, 21:58:20 ; Search time 11350 Seconds
(without alignments)
4653.408 Million cell updates/sec

Title: US-09-833-222A-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTPVPVLLGGNIRVYAL 1090

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_h/US09833222/runat_15112005_145358_15785/app_query.fasta_1.1287
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	5399.5	94.3	4604	9	AF516695	AF516695 Homo sapi
2	5386.5	94.1	5073	6	BD248445	BD248445 Alpha-2/d
3	5373.5	93.8	5359	9	HSM805741	BX537437 Homo sapi
4	5342.5	93.3	3339	6	AX098927	AX098927 Sequence
5	5342.5	93.3	3339	6	AX099347	AX099347 Sequence
6	5276	92.1	3209	6	AX098926	AX098926 Sequence
7	5276	92.1	3209	6	AX099346	AX099346 Sequence
8	5244.5	91.6	5001	6	BD248454	BD248454 Alpha-2/d
9	5239.5	91.5	5960	9	HSM805740	BX537436 Homo sapi
10	5214.5	91.1	5712	6	BD248455	BD248455 Alpha-2/d
11	5148	89.9	3201	6	AX098925	AX098925 Sequence
12	5148	89.9	3201	6	AX099345	AX099345 Sequence
13	3808	66.5	4125	6	AX302028	AX302028 Sequence
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15	3421.5	59.8	3276	10	AF486278	AF486278 Rattus no
16	3421.5	59.8	3544	9	HSA272268	AJ272268 Homo sapi
17	3416.5	59.7	3276	6	AR454329	AR454329 Sequence
18	3416.5	59.7	3276	6	AX427033	AX427033 Sequence
19	3416.5	59.7	3653	9	AF516696	AF516696 Homo sapi
20	3416.5	59.7	3690	6	AR454328	AR454328 Sequence
21	3416.5	59.7	3690	6	AX427031	AX427031 Sequence
22	3410.5	59.6	3770	6	BD248444	BD248444 Alpha-2/d
23	3410.5	59.6	3770	6	AX098896	AX098896 Sequence
24	3410.5	59.6	3770	6	AX099316	AX099316 Sequence
25	3400.5	59.4	3213	6	AX098884	AX098884 Sequence
26	3400.5	59.4	3213	6	AX099304	AX099304 Sequence
27	3326.5	58.1	3114	6	AX098883	AX098883 Sequence
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29	3297	57.6	3464	9	HSA272213	AJ272213 Homo sapi
30	3278.5	57.3	3057	6	AX098882	AX098882 Sequence
31	3278.5	57.3	3057	6	AX099302	AX099302 Sequence
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34	1868.5	32.6	2944	9	HSM801956	AL137658 Homo sapi
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36	1792.5	31.3	1050	6	AX099310	AX099310 Sequence
37	1695	29.6	969	6	AX098889	AX098889 Sequence
38	1695	29.6	969	6	AX099309	AX099309 Sequence
39	1598	27.9	912	6	AX098888	AX098888 Sequence
40	1598	27.9	912	6	AX099308	AX099308 Sequence
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42	1497.5	26.2	5862	6	AX155081	AX155081 Sequence
43	1410	24.6	6519	6	CQ602907	CQ602907 Sequence
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45	1336.5	23.3	3414	6	CQ585735	CQ585735 Sequence

ALIGNMENTS

RESULT 1
AF516695
LOCUS AF516695 4604 bp mRNA linear PRI 10-SEP-2002
DEFINITION Homo sapiens voltage-gated calcium channel alpha(2)delta-4 subunit mRNA, complete cds.
ACCESSION AF516695
VERSION AF516695.1 GI:22770593
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4604)
AUTHORS Qin,N., Yagel,S., Momplaisir,M.L., Codd,E.E. and D'Andrea,M.R.
TITLE Molecular Cloning and Characterization of the Human Voltage-Gated Calcium Channel alpha(2)delta-4 Subunit
JOURNAL Mol. Pharmacol. 62 (3), 485-496 (2002)
MEDLINE 22169250
PUBMED 12181424
REFERENCE 2 (bases 1 to 4604)
AUTHORS Qin,N., Yagel,S., Momplaisir,M.L., Codd,E.E. and D'Andrea,M.R.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Drug Discovery, Johnson & Johnson Pharmaceutical Research and Development L.L.C., McKean & Welsh Roads, Spring House, PA 19477, USA
FEATURES Location/Qualifiers
source 1. .4604
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ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          4604
Score:                    5399.50        Matches:         1037
Percent Similarity:       97.65%         Conservative:    4
Best Local Similarity:    97.28%         Mismatches:      25
Query Match:              94.30%         Indels:          1
DB:                       9              Gaps:            0

US-09-833-222A-10 (1-1090) x AF516695 (1-4604)

Qy          11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
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Db         586 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 645

Qy          31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
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Db         646 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 705

Qy          51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
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Db         706 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 765

Qy          71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
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Db         766 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 825

Qy          91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
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Qy         111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
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Qy         171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
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Qy         191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
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Qy         211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
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Qy         231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
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Qy         271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
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Qy         311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
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Qy         331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
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Qy         371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
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Qy         451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
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Qy         491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
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Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
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Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
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Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Qy        651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
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Qy        811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
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Qy        831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
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Qy        851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
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Qy        871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890
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Qy        891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910
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Db       3226 GTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTG 3285

Qy        911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3286 TTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGT 3345

Qy        931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3346 GTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAG 3405

Qy        951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
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Db       3406 TACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGG 3465

Qy        971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990
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Db       3466 CCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTG 3525

Qy        991 ThrAspProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluVal 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3526 ACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGTC 3585

Qy       1011 LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgPro 1030
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Db       3586 AAATATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACCA 3645

Qy       1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGly 1050
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Db       3646 GACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGCGGCGCCTCGGAC 3705

Qy       1051 PheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
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Db       3706 ACCTCAGCCTCGCCGCCCCTACTCCTGCT-GCCTGTGTGTGCCTGGGGGCTACTGCCCCA 3764

Qy       1071 MetProMetAsnThrPro 1076
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Db       3765 ACTCCTGCGGTGACACCA 3782
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RESULT 2
BD248445
LOCUS       BD248445               5073 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Alpha-2/delta gene.
ACCESSION   BD248445
VERSION     BD248445.1  GI:33058215
KEYWORDS    JP 2002526100-A/3.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5073)
  AUTHORS   Johns,M.A., Moldover,B. and Offord,J.D.
  TITLE     Alpha-2/delta gene
  JOURNAL   Patent: JP 2002526100-A 3 20-AUG-2002;
            WARNER LAMBERT CO
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002526100-A/3
            PD   20-AUG-2002
            PF   07-OCT-1999 JP 2000574561
            PR   07-OCT-1998 US    60/103322,30-OCT-1998 US    60/106473 PR
            29-DEC-1998 US    60/114088
            PI   MARGARET ANN JOHNS,BRIAN MOLDOVER,JAMES DAVID OFFORD PC
            C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P25/06,A61P25/08, PC
            A61P25/16,
            PC   A61P25/20,A61P25/22,A61P25/28,A61P25/30,A61P29/00,A61P35/00,
            PC   C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/
            PC   02,C12Q1/68,
            PC   G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
            Alpha-2/delta gene
            FH   Key             Location/Qualifiers
            FT   source          1. .5073
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FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          5073
Score:                    5386.50        Matches:         1035
Percent Similarity:       97.47%         Conservative:    4
Best Local Similarity:    97.09%         Mismatches:      27
Query Match:              94.07%         Indels:          1
DB:                       6              Gaps:            0

US-09-833-222A-10 (1-1090) x BD248445 (1-5073)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
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Db        294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
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Db        354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
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Db        414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
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Db        474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
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Db        534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
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Db        594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653

Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
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Db        654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713

Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
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Db        714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773

Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
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Db        774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
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Db        834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893

Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013

Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073

Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133

Qy        331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
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Db       1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193

Qy        351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253

Qy        371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
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Db       1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313

Qy        391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
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Db       1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373

Qy        411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
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Qy        431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
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Db       1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493

Qy        451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
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Db       1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
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Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
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Qy        511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
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Qy        531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
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Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
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Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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Db       1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913

Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
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Db       1914 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1973

Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Db       1974 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033

Qy        631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
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Db       2034 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2093
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Qy       651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
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Db      2094 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2153

Qy       671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
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Db      2154 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2213

Qy       691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
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Qy       711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
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Qy       731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750
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Qy       751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
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Qy       791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
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Qy       811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
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Qy       831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
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Qy       851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
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Qy       871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890
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Qy       891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910
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Qy       931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
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Qy       951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
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Qy       971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990
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Qy       991 ThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010
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Qy      1011 LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgPro 1030
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Qy      1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGly 1050
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Qy      1051 PheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
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Qy      1071 MetProMetAsnThrPro 1076
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RESULT 3
HSM805741

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LOCUS       HSM805741              5359 bp    mRNA    linear   PRI 16-JUN-2003
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686O0495 (from clone DKFZp686O0495);
            complete cds.
ACCESSION   BX537437
VERSION     BX537437.1  GI:31873375
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5359)
  AUTHORS   Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686O0495) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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Best Local Similarity:  96.90%      Mismatches:     29
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US-09-833-222A-10 (1-1090) x HSM805741 (1-5359)

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Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
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Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
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Db       2135 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 2194

Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
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Db       2195 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 2254
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Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Qy        631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
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Qy        651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
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RESULT 4
AX098927
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DEFINITION Sequence 52 from Patent WO0119870.
ACCESSION AX098927
VERSION AX098927.1 GI:13538144
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brown,J.P. and Bertelli,F.
TITLE Secreted soluble _g(a)2_g(d)-2, _g(a)2_g(d)-3 or _g(a)2_g(d)-4 calcium channel subunit polypeptides and screening assays using same
JOURNAL Patent: WO 0119870-A 52 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
FEATURES Location/Qualifiers
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ORIGIN

Alignment Scores:

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Percent Similarity:	97.54%	Conservative:	2
Best Local Similarity:	97.35%	Mismatches:	8
Query Match:	93.30%	Indels:	18
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US-09-833-222A-10 (1-1090) x AX098927 (1-3339)

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Db        354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
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Db        834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893

Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
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Db        894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
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Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
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Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
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Qy        371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
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Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
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Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
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Qy        511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
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Qy        531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
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Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
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Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Qy        691 ValAspMetAlaPheLeuGlyThrArgAla---------------------------- 700
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Qy        701 ------------------GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
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Qy        714 lSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
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DEFINITION  Sequence 52 from Patent WO0120336.
ACCESSION   AX099347
VERSION     AX099347.1  GI:13538490
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bertelli,F., Brown,J.P., Dissanayake,V., Suman-Chauhan,N. and
            Gee,N.S.
  TITLE     Screening for alpha2delta-1 subunit binding ligands
  JOURNAL   Patent: WO 0120336-A 52 22-MAR-2001;
            WARNER-LAMBERT COMPANY (US)
FEATURES             Location/Qualifiers
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Best Local Similarity:    97.35%           Mismatches:      8
Query Match:              93.30%           Indels:          18
DB:                       6                Gaps:            2

US-09-833-222A-10 (1-1090) x AX099347 (1-3339)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
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Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
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Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
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Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
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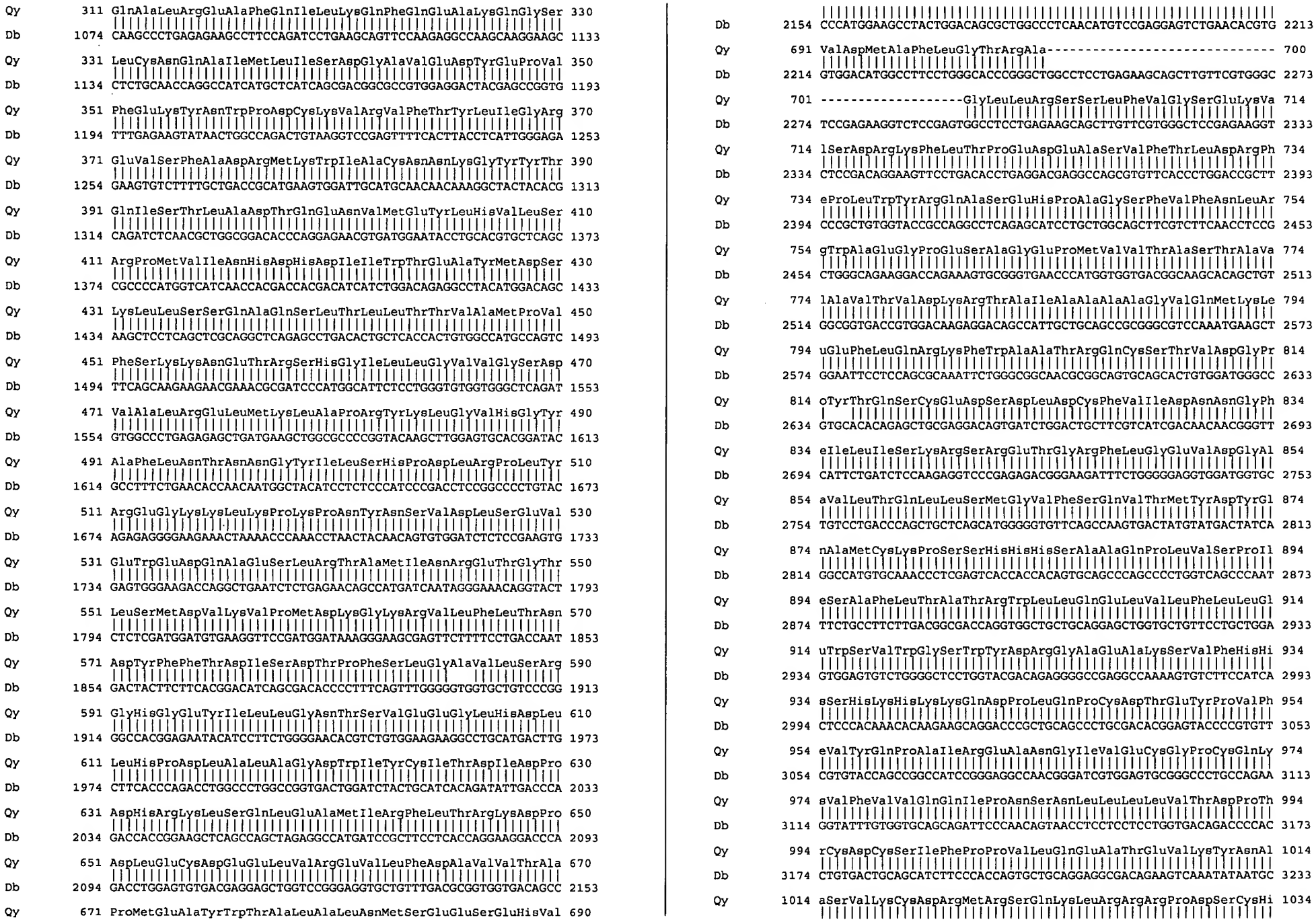
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Qy 754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
Db 2454 CTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGT 2513
Qy 774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLe 794
Db 2514 GGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCT 2573
Qy 794 uGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814
Db 2574 GGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCC 2633
Qy 814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPh 834
Db 2634 GTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGACAACAACGGGTT 2693
Qy 834 eIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854
Db 2694 CATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGC 2753
Qy 854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
Db 2754 TGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCA 2813
Qy 874 nAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuValSerProIl 894
Db 2814 GGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAAT 2873
Qy 894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGl 914
Db 2874 TTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGA 2933
Qy 914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHi 934
Db 2934 GTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCA 2993
Qy 934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
Db 2994 CTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTT 3053
Qy 954 eValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLy 974
Db 3054 CGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAA 3113
Qy 974 sValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProTh 994
Db 3114 GGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCAC 3173
Qy 994 rCysAspCysSerIleProProValLeuGlnGluAlaThrGluValLysTyrAsnAl 1014
Db 3174 CTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGC 3233
Qy 1014 aSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgProAspSerCysHi 1034

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Db       3234 CTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACCAGACTCCTGCCA 3293

Qy       1034 sAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
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Db       3294 CGCCTTCCATCCAGAGGAGAATGCCCAG---GACTGCGGCGGCGCC 3336

RESULT 6
AX098926
LOCUS       AX098926               3209 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 51 from Patent WO0119870.
ACCESSION   AX098926
VERSION     AX098926.1  GI:13538143
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Brown,J.P. and Bertelli,F.
  TITLE     Secreted soluble _g(a)2_g(d)-2, _g(a)2_g(d)-3 or _g(a)2_g(d)-4
            calcium channel subunit polypeptides and screening assays using
            same
  JOURNAL   Patent: WO 0119870-A 51 22-MAR-2001;
            WARNER-LAMBERT COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .3209
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          3209
Score:                    5276.00        Matches:         1008
Percent Similarity:       99.70%         Conservative:    1
Best Local Similarity:    99.60%         Mismatches:      3
Query Match:              92.14%         Indels:          0
DB:                       6              Gaps:            0

US-09-833-222A-10 (1-1090) x AX098926 (1-3209)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
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Db        594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653

Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
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Db        654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713

Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773

Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
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Db        834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893

Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013

Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073

Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133

Qy        331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193

Qy        351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
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Db       1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253

Qy        371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
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Db       1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313

Qy        391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
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Db       1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373

Qy        411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433

Qy        431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493

Qy        451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
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Db       1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
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Db       1554 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613

Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1614 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1673

Qy        511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1674 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1733

Qy        531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
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Db       1734 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1793

Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570

Db       1794 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 1853

Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590

Db       1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913

Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610

Db       1914 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1973

Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630

Db       1974 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033

Qy        631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650

Db       2034 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2093

Qy        651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670

Db       2094 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2153

Qy        671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690

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Qy        691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710

Db       2214 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2273

Qy        711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730

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Qy        731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750

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Qy        751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770

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Qy        771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyVal 790

Db       2454 AGCACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTC 2513

Qy        791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810

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Qy        811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830

Db       2574 GTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGAC 2633

Qy        831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850

Db       2634 AACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 2693

Qy        851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870

Db       2694 GTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATG 2753

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Qy        911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930

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Db       2994 TACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGG 3053

Qy        971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990

Db       3054 CCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTG 3113

Qy        991 ThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010

Db       3114 ACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGTC 3173

Qy       1011 LysTyrAsnAlaSerValLysCysAspArgMetArg 1022

Db       3174 AAATATAATGCCTCTGTCAAATGTGACCGGATGCGC 3209

RESULT 7
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LOCUS       AX099346               3209 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 51 from Patent WO0120336.
ACCESSION   AX099346
VERSION     AX099346.1  GI:13538489
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bertelli,F., Brown,J.P., Dissanayake,V., Suman-Chauhan,N. and
            Gee,N.S.
  TITLE     Screening for alpha2delta-1 subunit binding ligands
  JOURNAL   Patent: WO 0120336-A 51 22-MAR-2001;
            WARNER-LAMBERT COMPANY (US)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              0              Length:          3209
Score:                  5276.00        Matches:         1008
Percent Similarity:     99.70%         Conservative:    1
Best Local Similarity:  99.60%         Mismatches:      3
Query Match:            92.14%         Indels:          0
DB:                     6              Gaps:            0

US-09-833-222A-10 (1-1090) x AX099346 (1-3209)

Qy          11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30

Db         174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy          31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50

Db         234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy          51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70

Db         294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy          71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
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Db        354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110

Db        414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130

Db        474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150

Db        534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170

Db        594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653

Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190

Db        654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713

Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210

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Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230

Db        774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250

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Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270

Db        894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290

Db        954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013

Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310

Db       1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073

Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330

Db       1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133

Qy        331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350

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Db       1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253

Qy        371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390

Db       1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313

Qy        391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410

Db       1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373

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Db       1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433

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Db       1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493

Qy        451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470

Db       1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490

Db       1554 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613

Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510

Db       1614 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1673

Qy        511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530

Db       1674 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1733

Qy        531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550

Db       1734 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1793

Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570

Db       1794 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 1853

Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590

Db       1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913

Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610

Db       1914 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1973

Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630

Db       1974 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033

Qy        631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650

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Qy        651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670

Db       2094 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2153

Qy        671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690

Db       2154 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2213

Qy        691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710

Db       2214 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2273

Qy        711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730

Db       2274 TCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACC 2333

Qy        731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750

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Qy        831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
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Db       2634 AACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 2693

Qy        851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
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Qy        871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890
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Qy        891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910
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Db       2814 GTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTG 2873

Qy        911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
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Db       2874 TTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGT 2933

Qy        931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
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Qy        951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
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Qy        991 ThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010
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RESULT 8
BD248454
LOCUS       BD248454                5001 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Alpha-2/delta gene.
ACCESSION   BD248454
VERSION     BD248454.1  GI:33058224
KEYWORDS    JP 2002526100-A/12.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5001)
  AUTHORS   Johns,M.A., Moldover,B. and Offord,J.D.
  TITLE     Alpha-2/delta gene
  JOURNAL   Patent: JP 2002526100-A 12 20-AUG-2002;
            WARNER LAMBERT CO
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002526100-A/12
            PD   20-AUG-2002
            PF   07-OCT-1999 JP 2000574561
            PR   07-OCT-1998 US    60/103322,30-OCT-1998 US    60/106473 PR
            29-DEC-1998 US    60/114088
            PI   MARGARET ANN JOHNS,BRIAN MOLDOVER,JAMES DAVID OFFORD PC
            C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P25/06,A61P25/08, PC
            A61P25/16,
            PC   A61P25/20,A61P25/22,A61P25/28,A61P25/30,A61P29/00,A61P35/00,
            PC   C07K14/47,
            PC   C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/
            PC   02,C12Q1/68,
            PC   G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
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            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:          5001
Score:                  5244.50        Matches:         1011
Percent Similarity:     95.22%         Conservative:    4
Best Local Similarity:  94.84%         Mismatches:      27
Query Match:            91.59%         Indels:          25
DB:                     6              Gaps:            1

US-09-833-222A-10 (1-1090) x BD248454 (1-5001)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
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Db        294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
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Db        354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
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Db        474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
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Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
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Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
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Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
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Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
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Db        774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
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Db        834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893

Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
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Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
Db        954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013
Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
Db       1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073
Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db       1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133
Qy        331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db       1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193
Qy        351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db       1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253
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RESULT 9
HSM805740
LOCUS       HSM805740               5960 bp    mRNA    linear   PRI 16-JUN-2003
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686A1395 (from clone DKFZp686A1395).
ACCESSION   BX537436
VERSION     BX537436.1  GI:31873373
KEYWORDS    .
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5960)
  AUTHORS   Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686A1395) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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US-09-833-222A-10 (1-1090) x HSM805740 (1-5960)

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Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
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Qy       231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
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Qy       311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db      1317 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1376

Qy       331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
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Qy       351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db      1437 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1496

Qy       371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db      1497 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1556

Qy       391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
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Qy       471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
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Qy       491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
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Qy       531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
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Qy       571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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Qy       671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
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Qy       691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
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Qy       731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750
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Qy       811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
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Qy       831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
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Qy       910 ---------- 910
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Db       3237 AGGAGGGCACAATCCCTGGGCATGGACGCCACCTCTTCCCTGCATGCTGCCCCTGGGAGG 3296

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Qy        910 ------------------------------------------------------------ 910

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Qy        938 sLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnPr 958
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Db       3837 CAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCC 3896

Qy        958 oAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValVa 978
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Db       3957 GCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAG 4016

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Qy       1038 oGluValArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCy 1058
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Qy       1058 sLeuGlyLeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrPro 1076
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RESULT 10
BD248455
LOCUS       BD248455               5712 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Alpha-2/delta gene.
ACCESSION   BD248455
VERSION     BD248455.1  GI:33058225
KEYWORDS    JP 2002526100-A/13.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5712)
  AUTHORS   Johns,M.A., Moldover,B. and Offord,J.D.
  TITLE     Alpha-2/delta gene
  JOURNAL   Patent: JP 2002526100-A 13 20-AUG-2002;
            WARNER LAMBERT CO
COMMENT     OS   Homo sapiens (human)
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            PD   20-AUG-2002
            PF   07-OCT-1999 JP 2000574561
            PR   07-OCT-1998 US    60/103322,30-OCT-1998 US    60/106473 PR
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            PI   MARGARET ANN JOHNS,BRIAN MOLDOVER,JAMES DAVID OFFORD PC
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ORIGIN

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Percent Similarity:     81.02%         Conservative:   4
Best Local Similarity:  80.70%         Mismatches:     29
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US-09-833-222A-10 (1-1090) x BD248455 (1-5712)

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Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210

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Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270

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Db       1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433

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Db       1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493

Qy        451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470

Db       1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490

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Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510

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Qy       910 ------------------------------------------------------------ 910
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Qy       910 ------------------------------------------------------------ 910
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RESULT 11
AX098925
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DEFINITION  Sequence 50 from Patent WO0119870.
ACCESSION   AX098925
VERSION     AX098925.1  GI:13538142
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Brown,J.P. and Bertelli,F.
  TITLE     Secreted soluble _g(a)2_g(d)-2, _g(a)2_g(d)-3 or _g(a)2_g(d)-4
            calcium channel subunit polypeptides and screening assays using
            same
  JOURNAL   Patent: WO 0119870-A 50 22-MAR-2001;
            WARNER-LAMBERT COMPANY (US)
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ORIGIN

Alignment Scores:
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Score:                  5148.00         Matches:        989
Percent Similarity:     98.02%          Conservative:   1
Best Local Similarity:  97.92%          Mismatches:     3
Query Match:            89.91%          Indels:         17
DB:                     6               Gaps:           1

US-09-833-222A-10 (1-1090) x AX098925 (1-3201)

Qy        11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
             :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
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Qy        91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
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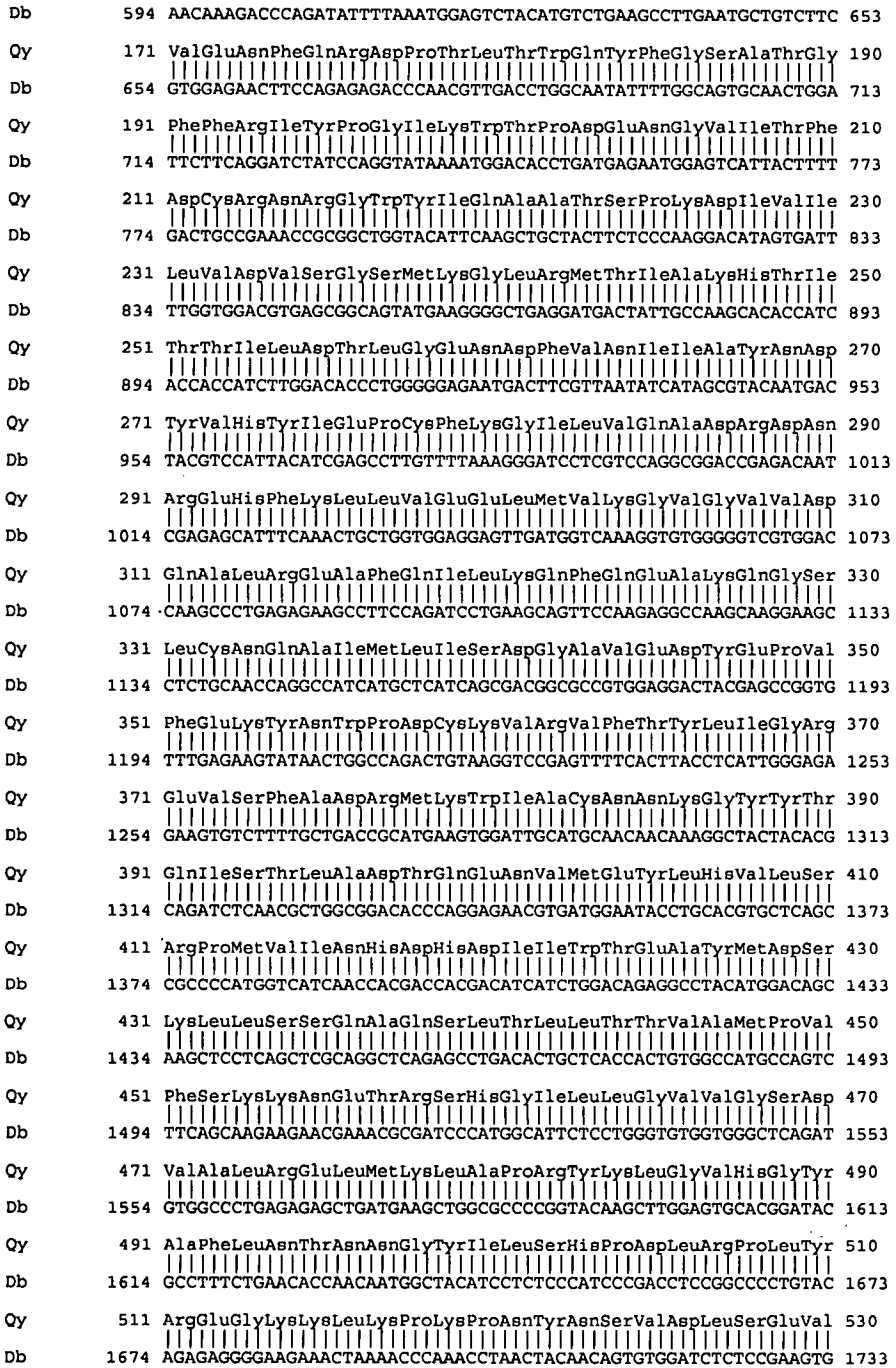
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Qy 191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
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Db 1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133
Qy 331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
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RESULT 12
AX099345
LOCUS       AX099345               3201 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 50 from Patent WO0120336.
ACCESSION   AX099345
VERSION     AX099345.1  GI:13538488
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bertelli,F., Brown,J.P., Dissanayake,V., Suman-Chauhan,N. and
            Gee,N.S.
  TITLE     Screening for alpha2delta-1 subunit binding ligands
  JOURNAL   Patent: WO 0120336-A 50 22-MAR-2001;
            WARNER-LAMBERT COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .3201
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:         3201
Score:                  5148.00        Matches:        989
Percent Similarity:     98.02%         Conservative:   1
Best Local Similarity:  97.92%         Mismatches:     3
Query Match:            89.91%         Indels:         17
DB:                     6              Gaps:           1

US-09-833-222A-10 (1-1090) x AX099345 (1-3201)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
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Db        414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
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Db        534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
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Db        594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653

Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
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Db        654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713

Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
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Db        714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773

Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
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Db        834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893

Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
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Db        894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
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Db        954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013

Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
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Db       1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073

Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
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Db       1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133

Qy        331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
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Db       1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193

Qy        351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
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Db       1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253

Qy        371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
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Db       1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313

Qy        391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
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Db       1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373

Qy        411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
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Qy       431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
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Qy       451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db      1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy       471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Db      1554 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613

Qy       491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
Db      1614 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1673

Qy       511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
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Qy       531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
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Qy       551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
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Qy       571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db      1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913

Qy       591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db      1914 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1973

Qy       611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Qy       631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
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Qy       651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
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Qy       671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
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Qy       691 ValAspMetAlaPheLeuGlyThrArgAla---------------------------- 700
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Qy       701 ------------------GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
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Qy       714 lSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
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Qy       734 eProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
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Qy       754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
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Qy       774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLe 794
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Db      2514 GGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCT 2573

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Qy       814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPh 834
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Qy       834 eIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854
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Qy       854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
Db      2754 TGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCA 2813

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Qy       894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGl 914
Db      2874 TTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGA 2933

Qy       914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHi 934
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Qy       934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
Db      2994 CTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTT 3053

Qy       954 eValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLy 974
Db      3054 CGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAA 3113

Qy       974 sValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProTh 994
Db      3114 GGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCAC 3173

Qy       994 rCysAspCysSerIleProProVal 1003
Db      3174 CTGTGACTGCAGCATCTTCCCACCAGTG 3201
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RESULT 13
AX302028
LOCUS       AX302028               4125 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 27 from Patent WO0177174.
ACCESSION   AX302028
VERSION     AX302028.1  GI:17383000
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Reddy,R., Thornton,M., Borowsky,M.L., Tang,Y.T., Khan,F.A.,
            Tribouley,C.M., Gandhi,A.R., Yao,M.G., Sanjanwala,M.S.,
            Baughn,M.R., Nguyen,D.B., Policky,J.L., Yue,H., Seilhamer,J.J.,
            Walia,N.K., Lal,P., Kearney,L., Walsh,R.T., Lu,D.A., Greene,B.D.,
            Raumann,B.E. and Patterson,C.
  JOURNAL   Patent: WO 0177174-A 27 18-OCT-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN
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Alignment Scores:
Pred. No.:              3.69e-280       Length:         4125
Score:                  3808.00         Matches:        750
Percent Similarity:     80.90%          Conservative:   4
Best Local Similarity:  80.47%          Mismatches:     14
Query Match:            66.50%          Indels:         164
DB:                     6               Gaps:           2

US-09-833-222A-10 (1-1090) x AX302028 (1-4125)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
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Db       1120 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 1179

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 1239

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 1299

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
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Db       1300 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 1359

Qy         91 HisGluPheAsnGluSerLeuVal---------------------------------- 98
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Db       1360 CACGAATTCAATGAATCCCTGGTGGAACCTGGCGTGGGAGTTGGCGTGGGGATGTCCGTG 1419

Qy         98 ---------------------------------------------------------- 98

Db       1420 ACGCAGTCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGACGCAGTCCGGCGTGGGAGTT 1479

Qy         98 ---------------------------------------------------------- 98

Db       1480 GGCGTGGGGATGTCCATAACGCTGTCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGAGG 1539

Qy         98 ---------------------------------------------------------- 98

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Qy         99 ----------------------------PheAspTyrTyrAsnSerValLeuIleAsnGlu 109
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Db       1840 TCCGTGGGCCTCACCCGTCCACCCCAGTTCGACTATTACAACTCGGTCCTGATCAACGAG 1899

Qy        110 ArgAspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAla 129
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Db       1900 AGGGACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCT 1959

Qy        130 HisPheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnVal 149
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Db       1960 CACTTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTG 2019

Qy        150 TyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaVal 169
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Db       2020 TACAACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTC 2079

Qy        170 PheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThr 189
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Db       2080 TTCGTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACT 2139

Qy        190 GlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThr 209
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Db       2140 GGATTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACT 2199

Qy        210 PheAspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleVal 229
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Db       2200 TTTGACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTG 2259

Qy        230 IleLeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThr 249
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Db       2260 ATTTTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACC 2319

Qy        250 IleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsn 269
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Db       2320 ATCACCACCATCTTGGACACCCTGGGGGAGAATGACTTCATTAATATCATAGCGTACAAT 2379

Qy        270 AspTyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAsp 289
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Qy        290 AsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValVal 309
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Db       2440 AATCGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTG 2499

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Qy        330 SerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluPro 349
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Db       2560 AGCCTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCG 2619

Qy        350 ValPheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGly 369
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Db       2620 GTGTTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGG 2679

Qy        370 ArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyr 389
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Db       2680 AGAGAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTAC 2739

Qy        390 ThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeu 409
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Db       2740 ACGCAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTC 2799

Qy        410 SerArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAsp 429
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Db       2800 AGCCGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGAC 2859

Qy        430 SerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetPro 449
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Db       2860 AGCAAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCA 2919

Qy        450 ValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySer 469
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Db       2920 GTCTTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCA 2979

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Qy        490 TyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu 509
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Qy        510 TyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGlu 529
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Db       3100 TACAGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAA 3159
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Qy        530 ValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGly 549
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Qy        550 ThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThr 569
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Db       3220 ACTCTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACC 3279

Qy        570 AsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSer 589
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Db       3280 AATGACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCC 3339

Qy        590 ArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAsp 609
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Qy        610 LeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAsp 629
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Qy        630 ProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAsp 649
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Qy        650 ProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThr 669
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Db       3520 CCAGACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACA 3579

Qy        670 AlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHis 689
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Qy        690 ValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheVal 709
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Qy        710 GlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPhe 729
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Qy        730 ThrLeuAspArgProProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
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Qy        750 ValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThr 769
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Qy        770 AlaSerThrAlaValAlaValThrValAspLysArg 781
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RESULT 14
MMU010949
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DEFINITION  Mus musculus mRNA for voltage gated calcium channel alpha-2-delta-C
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ACCESSION   AJ010949
VERSION     AJ010949.1  GI:4186072
KEYWORDS    calcium channel alpha-2-delta-C subunit.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Klugbauer,N., Lacinova,L., Marais,E., Hobom,M. and Hofmann,F.
  TITLE     Molecular diversity of the calcium channel alpha2delta subunit
  JOURNAL   J. Neurosci. 19, 648-691 (1999)
REFERENCE   2  (bases 1 to 3710)
  AUTHORS   Klugbauer,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-1998) Klugbauer N., Institut fuer Pharmakologie
            und Toxikologie, Technische Universitaet Muenchen, Biedersteiner
            Str. 29, 80802, GERMANY
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ORIGIN

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Percent Similarity:       77.37%          Conservative:    189
Best Local Similarity:    59.47%          Mismatches:      221
Query Match:              59.79%          Indels:          18
DB:                       10              Gaps:            6

US-09-833-222A-10 (1-1090) x MMU010949 (1-3710)

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Qy         33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
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Db        281 GGCTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAGGACGTTGCCATTGAAGAA 340

Qy         53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
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Db        341 ATCGACGGTCTCCAACTGGTGAAGAAGTTGGCTAAAATCATGGAGGAGATGTTCCACAAG 400

Qy         73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
              |||   |||||||||:::   |||||||||||||||||||||||   |||   ||||||
Db        401 AAGTCCGAGGCAGTGAGGCGTCTTGTGGAGGCTGCAGAGGAGGCACACCTGAAACATGAA 460

Qy         93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
              |||:::      |||   ::::::|||:::|||:::|||||||||||||||||||:::
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Qy        113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
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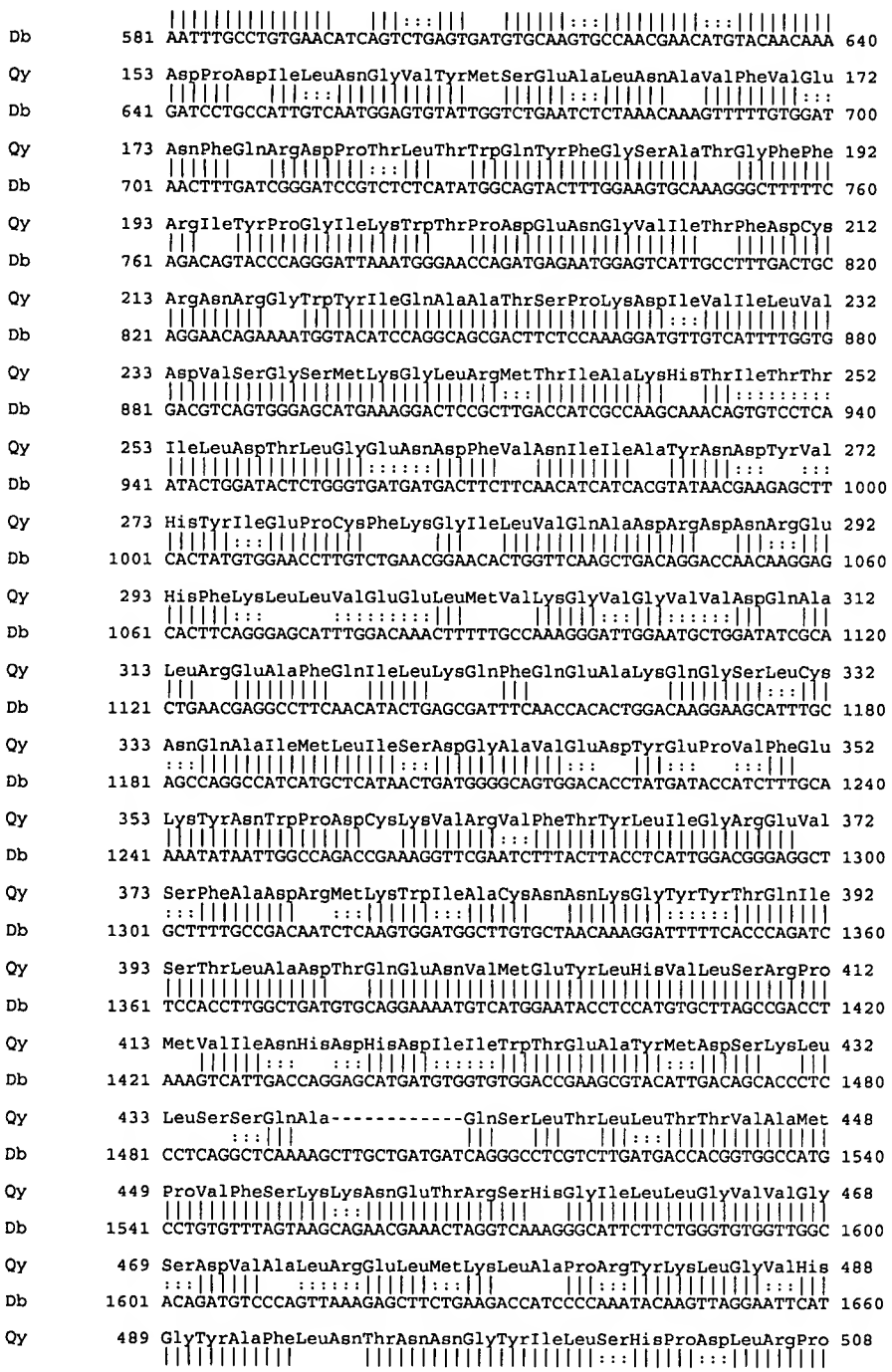

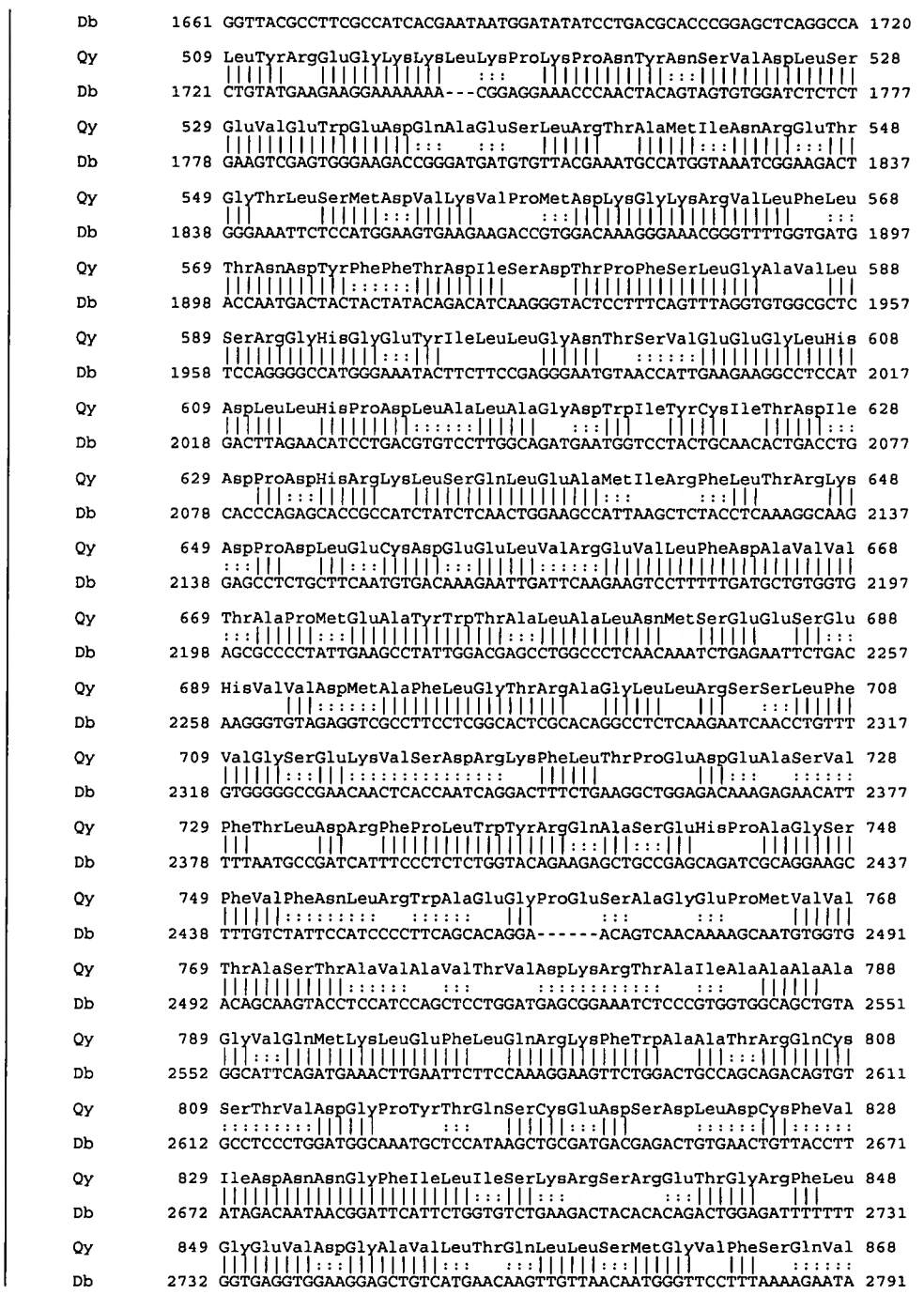

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Qy        929 LysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAsp 948
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Qy        969 CysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeu 988
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Db       3068 TGCGAAGACTGCTCCAAGTCCTTCGTCATCCAGCAAATCCCGAGTAGCAATCTGTTCATG 3127

Qy        989 LeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThr 1008
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Db       3128 GTGGTGGTGGACAGTAGCTGTCTCTGTGAGTCCGTGGCTCCTATAACCATGGCACCCATT 3187

Qy       1009 GluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArg 1028
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Db       3188 GAAATCAGGTATAATGAATCCCTTAAGTGTGAACGGTTAAAGGCTCAGAAGATCAGACGA 3247

Qy       1029 ArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrp 1048
              ||||||:::|||||||||   ||||||||||||                   |||
Db       3248 CGTCCAGAATCCTGCCACGGCTTCCATCCTGAGGAGAATGCAAGAGAGTGTGGGGGTGCA 3307

Qy       1049 AlaGly-PheSerSerProAsnProLeuCysLeuGlyLeuCysPro 1063
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Db       3308 TCGAGTCTTCAGGCCCAGGCGGCCTTGCTGC------TGCTGCCCC 3347
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RESULT 15
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LOCUS       AF486278               3276 bp    mRNA    linear   ROD 27-MAR-2003
DEFINITION  Rattus norvegicus calcium channel alpha-2 delta-3 subunit mRNA,
            complete cds.
ACCESSION   AF486278
VERSION     AF486278.1  GI:27450707
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 3276)
  AUTHORS   Chu,P.J. and Best,P.M.
  TITLE     Molecular cloning of calcium channel alpha(2)delta-subunits from
            rat atria and the differential regulation of their expression by
            IGF-1
  JOURNAL   J. Mol. Cell. Cardiol. 35 (2), 207-215 (2003)
  MEDLINE   22494975
   PUBMED   12606261
REFERENCE   2  (bases 1 to 3276)
  AUTHORS   Chu,P.-J. and Best,P.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-FEB-2002) Department of Molecular and Integrative
            Physiology, University of Illinois, 407 S. Goodwin Ave., Urbana, IL
            61801, USA
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ORIGIN

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US-09-833-222A-10 (1-1090) x AF486278 (1-3276)

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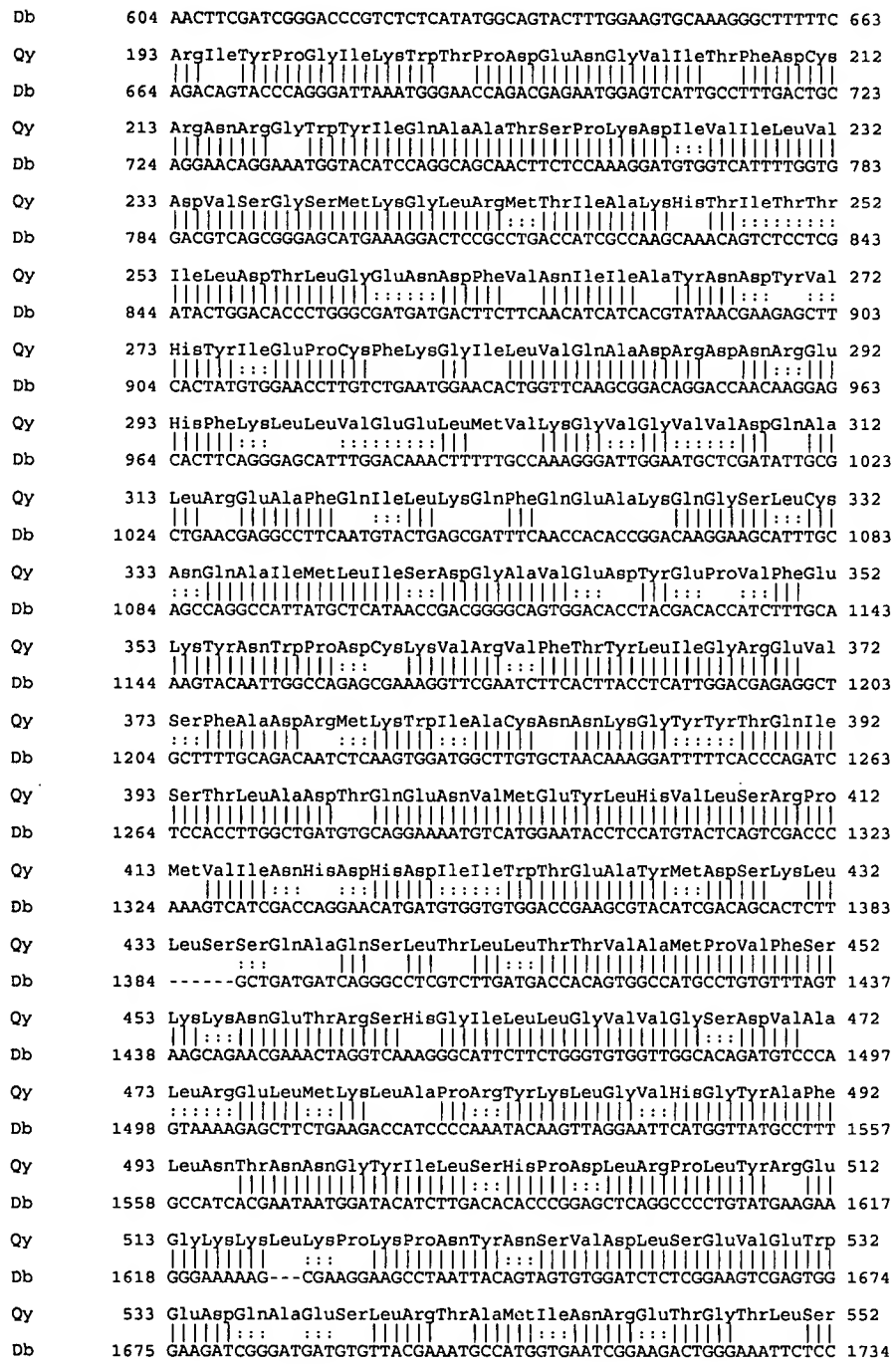
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Db 784 GACGTCAGCGGGAGCATGAAAGGACTCCGCCTGACCATCGCCAAGCAAACAGTCTCCTCG 843
Qy 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
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Db 1558 GCCATCACGAATAATGGATACATCTTGACACACCCGGAGCTCAGGCCCCTGTATGAAGAA 1617
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Qy       933 HisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrPro 952
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Job time : 11579 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 16, 2005, 03:13:23 ; Search time 45 Seconds
(without alignments)
1808.166 Million cell updates/sec

Title: US-09-833-222A-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTPVPVLLGGNIRVYAL 1090

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3422	59.8	1091	4	US-10-162-012-18	Sequence 18, Appl
2	3419.5	59.7	1077	4	US-09-397-550-24	Sequence 24, Appl
3	3416.5	59.7	1091	4	US-10-162-012-15	Sequence 15, Appl
4	3410.5	59.6	1065	4	US-09-397-550-12	Sequence 12, Appl
5	3410.5	59.6	1085	4	US-09-397-550-22	Sequence 22, Appl
6	3326.5	58.1	1038	4	US-09-397-550-11	Sequence 11, Appl
7	3278.5	57.3	1019	4	US-09-397-550-10	Sequence 10, Appl
8	1792.5	31.3	350	4	US-09-397-550-18	Sequence 18, Appl
9	1695	29.6	323	4	US-09-397-550-17	Sequence 17, Appl
10	1598	27.9	304	4	US-09-397-550-16	Sequence 16, Appl
11	1183.5	20.7	1076	4	US-09-470-443-6	Sequence 6, Appli
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20	1088	19.0	1106	1	US-08-336-257A-8	Sequence 8, Appli
21	1084	18.9	1084	1	US-08-455-543A-56	Sequence 56, Appl
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23	1079.5	18.9	1103	1	US-08-455-543A-53	Sequence 53, Appl
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25	1077.5	18.8	1091	1	US-07-745-206A-25	Sequence 25, Appl
26	1077.5	18.8	1091	1	US-08-455-543A-52	Sequence 52, Appl
27	1077.5	18.8	1091	2	US-08-223-305C-52	Sequence 52, Appl
28	1077.5	18.8	1091	2	US-08-311-363-25	Sequence 25, Appl
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32	1073.5	18.7	1091	3	US-08-713-118-4	Sequence 4, Appli
33	1073.5	18.7	1091	3	US-09-452-007-4	Sequence 4, Appli
34	1070	18.7	1086	1	US-08-455-543A-54	Sequence 54, Appl
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37	1023	17.9	1086	6	5386025-8	Patent No. 5386025
38	678	11.8	508	1	US-08-435-675B-6	Sequence 6, Appli
39	575	10.0	304	4	US-09-270-767-41584	Sequence 41584, A
40	460.5	8.0	173	4	US-10-000-489-100	Sequence 100, App
41	431	7.5	110	4	US-09-621-976-4028	Sequence 4028, Ap
42	294.5	5.1	127	4	US-09-621-976-5756	Sequence 5756, Ap
43	175	3.1	946	4	US-09-546-153-1	Sequence 1, Appli
44	174	3.0	946	3	US-09-074-579-3	Sequence 3, Appli
45	174	3.0	946	3	US-09-388-774-3	Sequence 3, Appli

ALIGNMENTS

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; Sequence 18, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11

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;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 1091
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-162-012-18

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;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 1077
;   TYPE: PRT
;   ORGANISM: Mus musculus
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Db        641 DLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVV 700

Qy        669 TAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASV 728
              :||:|||||:|||| || |:  |::|||||| || | :||||:|:::::: ||    |: ::
Db        701 SAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENI 760

Qy        729 FTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAA 788
              |  | ||||||:|:|  |||||::: :: |  :  :  ||||||:: :  :::: : ||
Db        761 FNADHFPLWYRRAAEQIAGSFVYSIPFSTG--TVNKSNVVTASTSIQLLDERKSPVVAAV 818

Qy        789 GVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFL 848
              |:|||||| ||||| |:|||:::||  : ||:|  ::|::|||||||:|:   :|| |
Db        819 GIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFF 878

Qy        849 GEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQEL 908
              |||:|||: :||:|| | ::|:|||||||: :     :|  |: |  |||:| :|:: ||
Db        879 GEVEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDSAHGLLDPYKAFLSAAKWIMTEL 938

Qy        909 VLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVE 968
              ||||:|:::  ||:     ||:        | :  |:|||||| || :  |:|  | :
Db        939 VLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIA 990

Qy        969 CGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRR 1028
              |  | |:|||:|||:||| ::| | :| |     |:     |::|| |:||:|:::||:||
Db        991 CEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKIRR 1050

Qy       1029 RPDSCHAFHPE 1039
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Db       1051 RPESCHGFHPE 1061
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RESULT 3
US-10-162-012-15
; Sequence 15, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-012-15

Query Match 59.7%; Score 3416.5; DB 4; Length 1091;
Best Local Similarity 60.3%; Pred. No. 0;
Matches 623; Conservative 188; Mismatches 203; Indels 19; Gaps 6;

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Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
              |||||  |||:: :   ||||| |||||||: |  : |||:|||:||:| :::|| |  :
Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKNMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
              | |||: |||||||| | |||:  | ::|:|:|||||||: |||:||| ||:|  | ||:
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
              ||||| |:| ||:|||:||||| |:|||| ||:|| |||:|| |||:| ||||||| |||
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
              | |||||| ||||||| ||||| ||||||||||:|||||||||||||:|||| |:::
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
              ||||||::|| |||||||: :|||:|||  | |||||| |:|||:  :::|  ||:|::| |
Db        282 ILDTLGDDDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
              | ||| ||  |     |||:|:||||||:||||: |: :| |||||| |||:||||||||
Db        342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
              :||| :||:|| |||::|||||||| ||||||||||||||| ||: :||::|||||:|| |
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQAQSLT------LLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLG 486
                 ||| ||      |:|||||||||:|||| |||||||:|| ::||:|  |:||||
Db        462 --PQAQKLTDDQGPVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLG 519

Qy        487 VHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINR 546
              :|||||  |||||||:||:|| || |||| : ||||:|||||||||||: : || ||:||
Db        520 IHGYAFAITNNGYILTHPELRLLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNR 578

Qy        547 ETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEG 606
              :||  ||:||  :||||||| :||||::|||  ||||||  ||||||:|   || ::|||
Db        579 KTGKFSMEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEG 638

Qy        607 LHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDA 666
              |||| |||::|| :| || ||: |:|| ||||||:  :|  |:| |:||:||::||||||
Db        639 LHDLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDA 698
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Qy        667 VVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEA 726
              ||:||:|||||:|||| || |:  |::|||||| || | :||||:|:::: ||   |:
Db        699 VVSAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKE 758

Qy        727 SVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAA 786
              ::|  | ||||||:|:|   ||||::: :: ||    :  ||||||:: :  :::: : |
Db        759 NIFNADHFPLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVVA 816

Qy        787 AAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGR 846
              | |:|||||| ||||| |:|||:::||  : ||:|  ::|::|||||||||:|:   :||
Db        817 AVGIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGD 876

Qy        847 FLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQ 906
              | ||::|||: :||:|| | ::|:|||||||: :      |  |: | :|||:| :|::
Db        877 FFGEIEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPYNAFLSAVKWIMT 936

Qy        907 ELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGI 966
              ||||||:|:::  ||:     ||:        | :  |:|||||| || :  |:|  |
Db        937 ELVLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGN 988

Qy        967 VECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKL 1026
              : |  | | ||:||||:||| ::| | :| |    |:     |::|| |:||:|:::||:
Db        989 IACEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKI 1048

Qy       1027 RRRPDSCHAFHPE 1039
              ||||:||| ||||
Db       1049 RRRPESCHGFHPE 1061


RESULT 4
US-09-397-550-12
; Sequence 12, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 1065
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-397-550-12

  Query Match            59.6%;  Score 3410.5;  DB 4;  Length 1065;
  Best Local Similarity  60.3%;  Pred. No. 0;
  Matches  619;  Conservative  188;  Mismatches  207;  Indels   13;  Gaps    5;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
              |||||  |||:: :   ||||| |||||||: |  : |||:|||:||:| :::|| |  :
Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKNMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
              | |||: |||||||| | |||:  | ::|:|:|||||||: |||:||| ||:|  | ||:
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
              |||||  |:| ||:|||:||||| |:|||| ||:|| |||:|| |||:| |||||| |||
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
              | |||||| ||||||| |||||| |||||||||||:|||||||||||||:|||| |:::
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
              ||||||:|| |||||: :||:|||  | |||||| |:|||:  :::|  ||:|::| |
Db        282 ILDTLGDDDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
              | ||| ||  |    |||:|:||||||:||||: |: :| |||||| |||:||||||||
Db        342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
              :||| :||:|| |||::|||||||| ||||||||||||||| ||: :||::|||||:|| |
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAF 492
                    |:|||||||||:||||| |||||||:|| ::||:|  |:||||:|||||
Db        462 TDDQGP--VLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLGIHGYAF 519

Qy        493 LNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLS 552
              |||||||:||:|| || |||| : ||||:||||||||||: : || ||:||:||  |
Db        520 AITNNGYILTHPELRLLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNRKTGKFS 578

Qy        553 MDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLLH 612
              |:||  :|||||| :||||::|||  ||||||  ||||||:|   || ::|||||| |
Db        579 MEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEGLHDLEH 638

Qy        613 PDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAPM 672
              ||::|| :| || ||: |:|| |||||:  :|  |:| |:||:||::||||||||:||:
Db        639 PDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVVSAPI 698

Qy        673 EAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLD 732
              |||||:|||| || |:  |::|||||| || | :||||:|:::: ||   |: ::|  |
Db        699 EAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENIFNAD 758

Qy        733 RFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQM 792
              ||||||:|:|   ||||::: :: ||    :  ||||||:: :  :::: : || |:||
Db        759 HFPLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVVAAVGIQM 816

Qy        793 KLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEVD 852
              |||| ||||| |:|||:::||  : ||:|  ::|::|||||||:|:   :|| | ||::
Db        817 KLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFFGEIE 876

Qy        853 GAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFL 912
              |||: :||:|| | ::|:|||||||: :      |  |: | :|||:| :|:: ||||||
Db        877 GAVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPYNAFLSAVKWIMTELVLFL 936

Qy        913 LEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECGPC 972
              :|:::  ||:     ||:        | :  |:|||||| || :  |:|  | : | |
Db        937 VEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIACEDC 988

Qy        973 QKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRPDS 1032
              | ||:||||:||| ::| | :| |    |:     |::|| |:||:|:::||:||||:|
Db        989 SKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKIRRRPES 1048

Qy       1033 CHAFHPE 1039
              || ||||
Db       1049 CHGFHPE 1055


RESULT 5
US-09-397-550-22
; Sequence 22, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 1085
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-397-550-22
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  Query Match           59.6%;  Score 3410.5;  DB 4;  Length 1085;
  Best Local Similarity  60.3%;  Pred. No. 0;
  Matches  619;  Conservative  188;  Mismatches  207;  Indels   13;  Gaps    5;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKNMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
Db        282 ILDTLGDDDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
Db        342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAF 492
Db        462 TDDQGP--VLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLGIHGYAF 519

Qy        493 LNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLS 552
Db        520 AITNNGYILTHPELRLLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNRKTGKFS 578

Qy        553 MDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLLH 612
Db        579 MEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEGLHDLEH 638

Qy        613 PDLALAGDWIYCITDIPDPHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAPM 672
Db        639 PDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVVSAPI 698

Qy        673 EAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLD 732
Db        699 EAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENIFNAD 758

Qy        733 RFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQM 792
Db        759 HFPLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVVAAVGIQM 816

Qy        793 KLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEVD 852
Db        817 KLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFFGEIE 876

Qy        853 GAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFL 912
Db        877 GAVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPYNAFLSAVKWIMTELVLFL 936

Qy        913 LEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECGPC 972
Db        937 VEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIACEDC 988

Qy        973 QKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRPDS 1032
Db        989 SKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKIRRRPES 1048

Qy       1033 CHAFHPE 1039
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Db       1049 CHGFHPE 1055


RESULT 6
US-09-397-550-11
; Sequence 11, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 1038
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-397-550-11

  Query Match           58.1%;  Score 3326.5;  DB 4;  Length 1038;
  Best Local Similarity  60.0%;  Pred. No. 0;
  Matches  606;  Conservative  185;  Mismatches  206;  Indels   13;  Gaps    5;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKNMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
Db        282 ILDTLGDDDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
Db        342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAF 492
Db        462 TDDQGP--VLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLGIHGYAF 519

Qy        493 LNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLS 552
Db        520 AITNNGYILTHPELRLLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNRKTGKFS 578

Qy        553 MDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLLH 612
Db        579 MEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEGLHDLEH 638

Qy        613 PDLALAGDWIYCITDIPDPHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAPM 672
Db        639 PDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVVSAPI 698

Qy        673 EAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLD 732
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Db        699 EAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENIFNAD 758

Qy        733 RFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQM 792

Db        759 HFPLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVVAAVGIQM 816

Qy        793 KLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEVD 852

Db        817 KLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFFGEIE 876

Qy        853 GAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFL 912

Db        877 GAVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPYNAFLSAVKWIMTELVLFL 936

Qy        913 LEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECGPC 972

Db        937 VEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIACEDC 988

Qy        973 QKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMR 1022

Db        989 SKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLK 1038


RESULT 7
US-09-397-550-10
; Sequence 10, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 1019
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-397-550-10

  Query Match             57.3%;  Score 3278.5;  DB 4;  Length 1019;
  Best Local Similarity   60.4%;  Pred. No. 2.9e-315;
  Matches  599;  Conservative  179;  Mismatches  200;  Indels   13;  Gaps    5;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72

Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKNMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132

Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192

Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252

Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312

Db        282 ILDTLGDDDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372

Db        342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432

Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAF 492

Db        462 TDDQGP--VLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLGIHGYAF 519

Qy        493 LNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLS 552

Db        520 AITNNGYILTHPELRLLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNRKTGKFS 578

Qy        553 MDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLLH 612

Db        579 MEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEGLHDLEH 638

Qy        613 PDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAPM 672

Db        639 PDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVVSAPI 698

Qy        673 EAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLD 732

Db        699 EAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENIFNAD 758

Qy        733 RFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQM 792

Db        759 HFPLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVVAAVGIQM 816

Qy        793 KLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEVD 852

Db        817 KLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFFGEIE 876

Qy        853 GAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFL 912

Db        877 GAVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPYNAFLSAVKWIMTELVLFL 936

Qy        913 LEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECGPC 972

Db        937 VEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIACEDC 988

Qy        973 QKVFVVQQIPNSNLLLLVTDPTCDCSIFPPV 1003

Db        989 SKSFVIQQIPSSNLFMVVVDSSCLCESVAPI 1019


RESULT 8
US-09-397-550-18
; Sequence 18, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 350
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-397-550-18

  Query Match             31.3%;  Score 1792.5;  DB 4;  Length 350;
  Best Local Similarity   97.4%;  Pred. No. 1.2e-168;
  Matches  341;  Conservative    2;  Mismatches    6;  Indels    1;  Gaps    1;

Qy        700 AGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGP 759

Db          1 SGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGP 60

Qy        760 ESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSC 819
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         61 ESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPCTQSC 120

Qy        820 EDSDLDCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EDSDLDCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 180

Qy        880 SSHHHSAAQPLVSPISAFLTATRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHK 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSHHHSAAQPLVSPISAFLTATRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHK 240

Qy        940 KQDPLQPCDTEYPVFVYQPAIREANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSI 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KQDPLQPCDTEYPVFVYQPAIREANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSI 300

Qy       1000 FPPVLQEATEVKYNASVKCDRMRSQKLRRRPDSCHAFHPEVRVEADRGWA 1049
              ||||||||||||||||||||||||||||||||||||||||   :  | | |
Db        301 FPPVLQEATEVKYNASVKCDRMRSQKLRRRPDSCHAFHPEENAQ-DCGGA 349


RESULT 9
US-09-397-550-17
; Sequence 17, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-397-550-17

  Query Match             29.6%;  Score 1695;  DB 4;  Length 323;
  Best Local Similarity   99.4%;  Pred. No. 4.9e-159;
  Matches  321;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        700 AGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGP 759
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGP 60

Qy        760 ESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSC 819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         61 ESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPCTQSC 120

Qy        820 EDSDLDCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EDSDLDCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 180

Qy        880 SSHHHSAAQPLVSPISAFLTATRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHK 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSHHHSAAQPLVSPISAFLTATRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHK 240

Qy        940 KQDPLQPCDTEYPVFVYQPAIREANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSI 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KQDPLQPCDTEYPVFVYQPAIREANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSI 300

Qy       1000 FPPVLQEATEVKYNASVKCDRMR 1022
              |||||||||||||||||||||||
Db        301 FPPVLQEATEVKYNASVKCDRMR 323


RESULT 10
US-09-397-550-16
; Sequence 16, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 304
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-397-550-16

  Query Match             27.9%;  Score 1598;  DB 4;  Length 304;
  Best Local Similarity   99.3%;  Pred. No. 1.8e-149;
  Matches  302;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        700 AGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGP 759
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGP 60

Qy        760 ESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSC 819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         61 ESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPCTQSC 120

Qy        820 EDSDLDCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EDSDLDCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 180

Qy        880 SSHHHSAAQPLVSPISAFLTATRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHK 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSHHHSAAQPLVSPISAFLTATRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHK 240

Qy        940 KQDPLQPCDTEYPVFVYQPAIREANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSI 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KQDPLQPCDTEYPVFVYQPAIREANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSI 300

Qy       1000 FPPV 1003
              ||||
Db        301 FPPV 304


RESULT 11
US-09-470-443-6
; Sequence 6, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
;  APPLICANT: Lerman, Michael I.
;  APPLICANT: Minna, John D.
;  APPLICANT: Latif, Farida
;  APPLICANT: Wei, Ming-Hui
;  APPLICANT: Sekido, Yoshitaka
;  APPLICANT: Gao, Boning
;  APPLICANT: Duh, Fuh-Mei
;  TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
;  FILE REFERENCE: NIH-05043
;  CURRENT APPLICATION NUMBER: US/09/470,443
;  CURRENT FILING DATE: 1999-12-22
;  EARLIER APPLICATION NUMBER: 60/114,359
;  EARLIER FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 1076
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-470-443-6

  Query Match             20.7%;  Score 1183.5;  DB 4;  Length 1076;
  Best Local Similarity   29.6%;  Pred. No. 2.7e-107;
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  Matches  343;  Conservative  209;  Mismatches  436;  Indels  169;  Gaps   42;

Qy         16 WADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRRKVE 75
Db          4 WARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFEVQENEPQKLVEKVAGDIESLLDRKVQ 63

Qy         76 AVQNLVEAAEEADLNHEFNESLVFD---YYNSVLINERDE-KGNFVELGA-------EFL 124
Db         64 ALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVERGSKASTLRLDFI 123

Qy        125 LESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQY 184
Db        124 EDPN--FKN-KVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRRQDPTLLWQV 180

Qy        185 FGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMT 244
Db        181 FGSATGVTRYYPATPWRAPKK-IDLYDVRRRPWYIQGASSPKDMVIIVDVSGSVSGLTLK 239

Qy        245 IAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVK 304
Db        240 LMKTSVCEMLDTLSDDDYVNVASFNEKAQPVS-CFTH-LVQANVRNKKVFKEAVQGMVAK 297

Qy        305 GVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVF 364
Db        298 GTTGYKAGFEYAFDQLQNSNITRAN--CNKMIMMFTDGGEDRVQDVFEKYNWPNRTVRVF 355

Qy        365 TYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVI--NHDHDII 422
Db        356 TFSVGQHNYDVTPLQWMACANKGYYFEIPSIGAIRINTQEYLDVLGRPMVLAGKEAKQVQ 415

Qy        423 WTEAYMDSKLLSSQAQSLTLLTTVAMPVFS--------KKNETRSHGILLGVVGSDVALR 474
Db        416 WTNVYED-------ALGLGLVVTGTLPVFNLTQDGPGEKKNQ-----LILGVMGIDVALN 463

Qy        475 ELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPL---YREGKKLKPKPNYNSVDLSEVE 531
Db        464 DIKRLTPNYTLGANGYVFAIDLNGYVLLHPNLKPQTTNFREPVTL---------DFLDAE 514

Qy        532 WEDQ-AESLRTAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSR 590
Db        515 LEDENKEEIRRSMIDGNKGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSLGLVLPP 574

Qy        591 GHGEYI---------------LLGNTSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRK 634
Db        575 YSTFYLQANLSDQILQVKYFEFLLPSSFESEG-HVFIAPR-------EYC-KDLNASDNN 625

Qy        635 LSQLEAMIRFLTRKDPD-LECDEELVREVLFDAVVTAPM-EAYWTALALNMSEESEHVVD 692
Db        626 TEFLKNFIELMEKVTPDSKQCNNFLLHNLILDTGITQQLVERVWRDQDLN-----TYSLL 680

Qy        693 MAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPL---WYRQASEHPAGSF 749
Db        681 AVFAATDGGITR--------------VFPNKAAEDWTENPEPFNASFYRRSLDN--HGY 723

Qy        750 VFN-------LRWAEGP-ESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKF 801
Db        724 VFKPPHQDALLR----PLELENDTVGILVSTAVELSLGRRTLRPAVVGVKLDLEAWAEKF 779

Qy        802 WAATRQCSTVDGPYTQSC------------EDSDLDCFVIDNNGFILISKRSR---ETGR 846
Db        780 KVLASNRTHQDQP--QKCGPNSHCEMDCEVNNEDLLCVLIDDGGFLVLSNQNHQWDQVGR 837

Qy        847 FLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQP---LVSPISAFL----- 898
Db        838 FFSEVDANLMLALYNNSFYTRKESYDYQAACAPQPPGNLGAAPRGVFVPTVADFLNLAWW 897

Qy        899 -TATRWLLQELVLFLLEWSVWGSWYDRG---AEAKSVFHHSHKHKKQDPLQPCDTEYPVF 954
Db        898 TSAAAWSLFQQLLYGL---IYHSWFQADPAEAEGSPETRESSCVMKQ-------TQY--- 944

Qy        955 VYQPAIREA-NGIVECGPCQKVFVVQQIPNSNLLLLVTD-PTCDCSIFPPVLQEATEVKY 1012
Db        945 -YFGSVNASYNAIIDCGNCSRLFHAQRLTNTNLLFVVAEKPLCSQCEAGRLLQKETHCPA 1003

Qy       1013 NASVKCDRMRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRQ--EHIG 1070
Db       1004 DGPEQCELVQRPRYRRGPHICFDYN----ATEDTSDCGRGASFPPSLGVLVSLQLLLLLG 1059

Qy       1071 MPMNTPVPVLLGGNIRV 1087
Db       1060 LPPRPQPQVLVHASRRL 1076


RESULT 12
US-09-470-443-2
; Sequence 2, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
;  APPLICANT: Lerman, Michael I.
;  APPLICANT: Minna, John D.
;  APPLICANT: Latif, Farida
;  APPLICANT: Wei, Ming-Hui
;  APPLICANT: Sekido, Yoshitaka
;  APPLICANT: Gao, Boning
;  APPLICANT: Duh, Fuh-Mei
;  TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
;  FILE REFERENCE: NIH-05043
;  CURRENT APPLICATION NUMBER: US/09/470,443
;  CURRENT FILING DATE: 1999-12-22
;  EARLIER APPLICATION NUMBER: 60/114,359
;  EARLIER FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1145
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-470-443-2

  Query Match           20.7%;  Score 1183.5;  DB 4;  Length 1145;
  Best Local Similarity   29.6%;  Pred. No. 3e-107;
  Matches  343;  Conservative  209;  Mismatches  436;  Indels  169;  Gaps   42;

Qy         16 WADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRRKVE 75
Db         73 WARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFEVQENEPQKLVEKVAGDIESLLDRKVQ 132

Qy         76 AVQNLVEAAEEADLNHEFNESLVFD---YYNSVLINERDE-KGNFVELGA-------EFL 124
Db        133 ALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVERGSKASTLRLDFI 192

Qy        125 LESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQY 184
Db        193 EDPN--FKN-KVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRRQDPTLLWQV 249

Qy        185 FGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMT 244
Db        250 FGSATGVTRYYPATPWRAPKK-IDLYDVRRRPWYIQGASSPKDMVIIVDVSGSVSGLTLK 308

Qy        245 IAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVK 304
Db        309 LMKTSVCEMLDTLSDDDYVNVASFNEKAQPVS-CFTH-LVQANVRNKKVFKEAVQGMVAK 366

Qy        305 GVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVF 364
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Qy        365 TYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVI--NHDHDII 422
Db        425 TFSVGQHNYDVTPLQWMACANKGYYFEIPSIGAIRINTQEYLDVLGRPMVLAGKEAKQVQ 484

Qy        423 WTEAYMDSKLLSSQAQSLTLLTTVAMPVFS--------KKNETRSHGILLGVVGSDVALR 474
Db        485 WTNVYED-------ALGLGLVVTGTLPVFNLTQDGPGEKKNQ-----LILGVMGIDVALN 532

Qy        475 ELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPL---YREGKKLKPKPNYNSVDLSEVE 531
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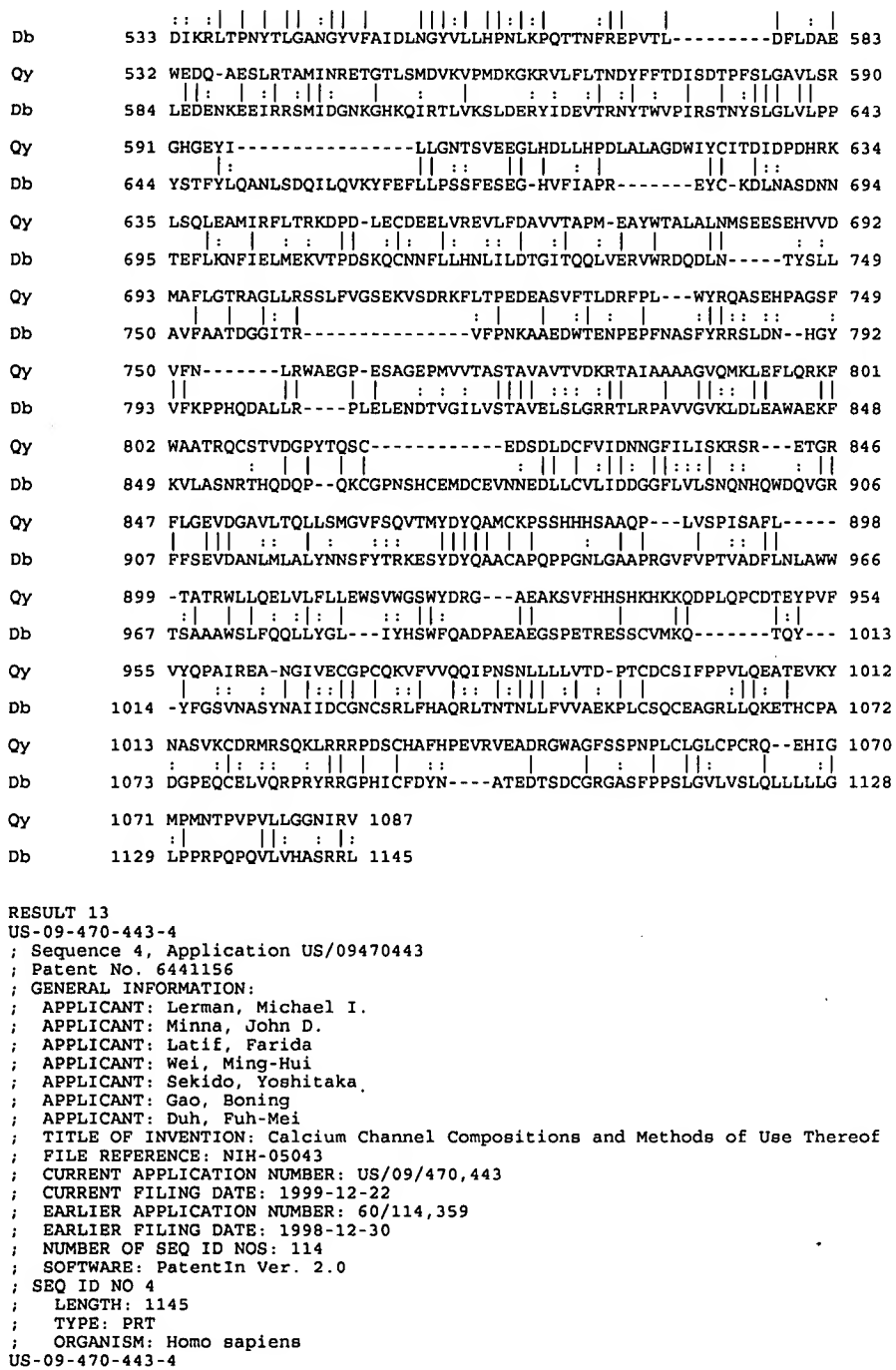
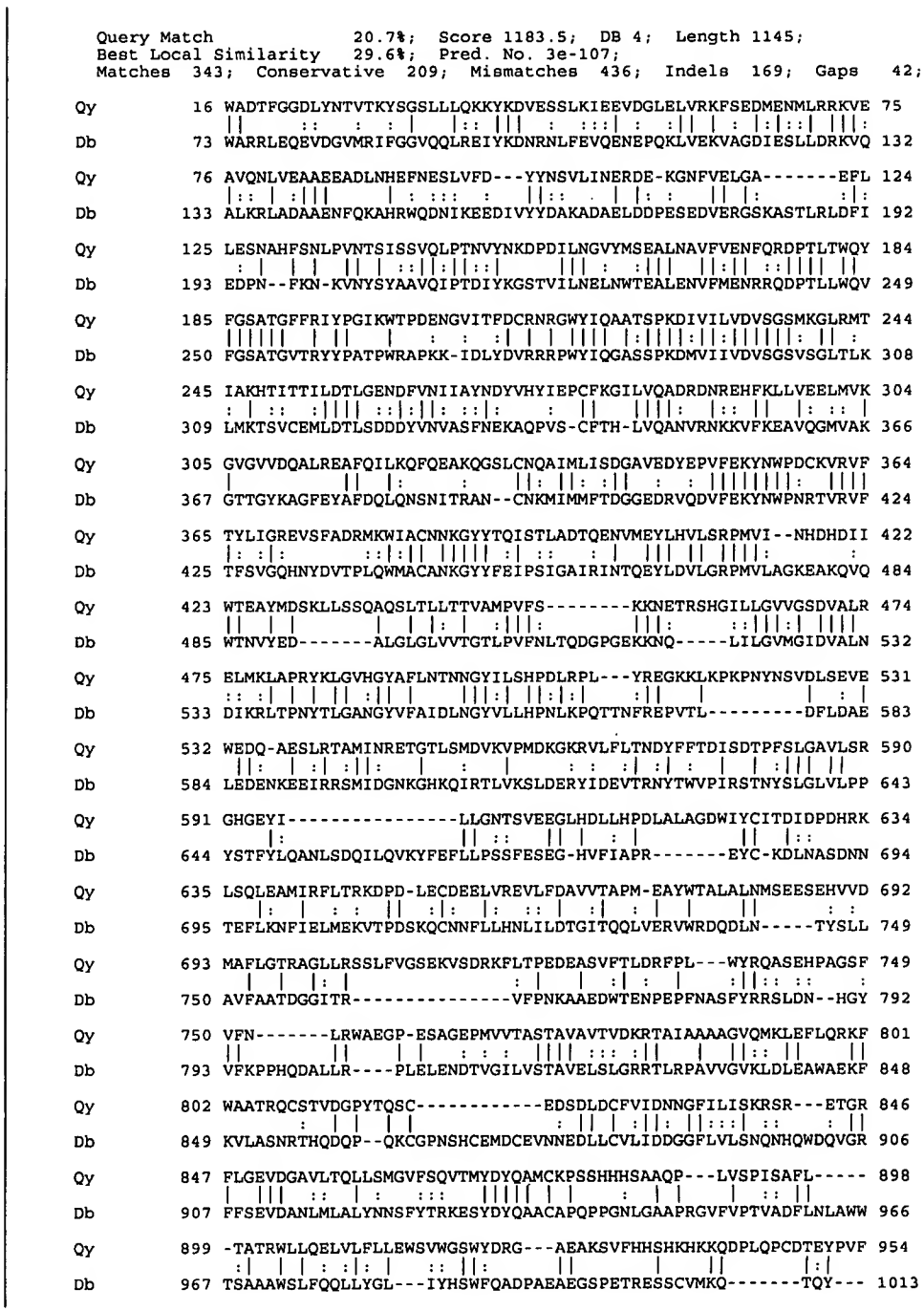


Query Match 20.7%; Score 1183.5; DB 4; Length 1145;
Best Local Similarity 29.6%; Pred. No. 3e-107;
Matches 343; Conservative 209; Mismatches 436; Indels 169; Gaps 42;



RESULT 13
US-09-470-443-4
; Sequence 4, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-470-443-4

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Qy       1013 NASVKCDRMRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRQ--EHIG 1070
              :  :|: :: : || |  |  ::     |   |  :  |  ||:   |    :|
Db       1073 DGPEQCELVQRPRYRRGPHICFDYN----ATEDTSDCGRGASFPPSLGVLVSLQLLLLLG 1128

Qy       1071 MPMNTPVPVLLGGNIRV 1087
              :|      ||:  : |:
Db       1129 LPPRPQPQVLVHASRRL 1145


RESULT 14
US-09-397-550-20
; Sequence 20, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 1145
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-397-550-20

  Query Match             20.7%;  Score 1183.5;  DB 4;  Length 1145;
  Best Local Similarity   29.6%;  Pred. No. 3e-107;
  Matches  343;  Conservative  209;  Mismatches  436;  Indels  169;  Gaps   42;

Qy         16 WADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRRKVE 75
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Db         73 WARRLEQEVDGVMRIFGGVQQLREIYKDNRNLFEVQENEPQKLVEKVAGDIESLLDRKVQ 132

Qy         76 AVQNLVEAAEEADLNHEFNESLVFD---YYNSVLINERDE-KGNFVELGA-------EFL 124
              |:: | :|||     | : :::  :   ||::    | |: :   || |:       :|:
Db        133 ALKRLADAAENFQKAHRWQDNIKEEDIVYYDAKADAELDDPESEDVERGSKASTLRLDFI 192

Qy        125 LESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQY 184
               : |  | |  || | ::||:||::|     ||| :  :|||  ||:|| ::|||| ||
Db        193 EDPN--FKN-KVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRRQDPTLLWQV 249

Qy        185 FGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMT 244
              ||||||  | ||   |   :  :  :| | | |||| |:||||:||:||||||: || :
Db        250 FGSATGVTRYYPATPWRAPKK-IDLYDVRRRPWYIQGASSPKDMVIIVDVSGSVSGLTLK 308

Qy        245 IAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVK 304
              : | ::  :|||| ::|:||: ::|:    :  ||   ||||:  |:: ||  |: : |
Db        309 LMKTSVCEMLDTLSDDDYVNVASFNEKAQPVS-CFTH-LVQANVRNKKVFKEAVQGMVAK 366

Qy        305 GVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVF 364
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Db        367 GTTGYKAGFEYAFDQLQNSNITRAN--CNKMIMMFTDGGEDRVQDVFEKYNWPNRTVRVF 424

Qy        365 TYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVI--NHDHDII 422
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Db        425 TFSVGQHNYDVTPLQWMACANKGYYFEIPSIGAIRINTQEYLDVLGRPMVLAGKEAKQVQ 484

Qy        423 WTEAYMDSKLLSSQAQSLTLLTTVAMPVFS--------KKNETRSHGILLGVVGSDVALR 474
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Db        485 WTNVYED-------ALGLGLVVTGTLPVFNLTQDGPGEKKNQ-----LILGVMGIDVALN 532

Qy        475 ELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPL---YREGKKLKPKPNYNSVDLSEVE 531
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Db        584 LEDENKEEIRRSMIDGNKGHKQIRTLVKSLDERYIDEVTRNYTWVPIRSTNYSLGLVLPP 643

Qy        591 GHGEYI----------------LLGNTSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRK 634
                 |:                || ::   || |  : |        ||  |::
Db        644 YSTFYLQANLSDQILQVKYFEFLLPSSFESEG-HVFIAPR-------EYC-KDLNASDNN 694

Qy        635 LSQLEAMIRFLTRKDPD-LECDEELVREVLFDAVVTAPM-EAYWTALALNMSEESEHVVD 692
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Db        695 TEFLKNFIELMEKVTPDSKQCNNFLLHNLILDTGITQQLVERVWRDQDLN-----TYSLL 749

Qy        693 MAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPL---WYRQASEHPAGSF 749
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Qy        802 WAATRQCSTVDGPYTQSC------------EDSDLDCFVIDNNGFILISKRSR---ETGR 846
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Db       1073 DGPEQCELVQRPRYRRGPHICFDYN----ATEDTSDCGRGASFPPSLGVLVSLQLLLLLG 1128

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; Sequence 6, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 1109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-397-550-6

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Db       193 EDPN--FKN-KVNYSYAAVQIPTDIYKGSTVILNELNWTEALENVFMENRRQDPTLLWQV 249

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Qy       635 LSQLEAMIRFLTRKDPD-LECDEELVREVLFDAVVTAPM-EAYWTALALNMSEESEHVVD 692
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Qy       802 WAATRQCSTVDGPYTQSC------------EDSDLDCFVIDNNGFILISKRSR---ETGR 846
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Qy       847 FLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQP---LVSPISAFL----- 898
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Qy       955 VYQPAIREA-NGIVECGPCQKVFVVQQIPNSNLLLLVTD-PTCDCSIFPPVLQEATEVKY 1012
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 16, 2005, 03:22:59 ; Search time 175 Seconds
(without alignments)
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5726	100.0	1090	14	US-10-119-624-10	Sequence 10, Appl
3	5385.5	94.1	1207	16	US-10-128-558-176	Sequence 176, App
4	5234.5	91.4	1075	15	US-10-257-174-34	Sequence 34, Appl
5	5230.5	91.3	1114	15	US-10-257-174-35	Sequence 35, Appl
6	3808	66.5	1310	15	US-10-257-022-12	Sequence 12, Appl
7	3422	59.8	1091	9	US-09-875-423-5	Sequence 5, Appli
8	3422	59.8	1091	14	US-10-162-012-18	Sequence 18, Appl
9	3422	59.8	1091	15	US-10-162-102-18	Sequence 18, Appl
10	3419.5	59.7	1077	17	US-10-902-531-24	Sequence 24, Appl
11	3416.5	59.7	1091	9	US-09-875-423-2	Sequence 2, Appli
12	3416.5	59.7	1091	14	US-10-162-012-15	Sequence 15, Appl
13	3416.5	59.7	1091	15	US-10-162-102-15	Sequence 15, Appl
14	3411	59.6	1091	17	US-10-924-081-6	Sequence 6, Appli
15	3410.5	59.6	1065	17	US-10-902-531-12	Sequence 12, Appl
16	3410.5	59.6	1085	17	US-10-902-531-22	Sequence 22, Appl
17	3410	59.6	1085	17	US-10-924-081-4	Sequence 4, Appli
18	3326.5	58.1	1038	17	US-10-902-531-11	Sequence 11, Appl
19	3278.5	57.3	1019	17	US-10-902-531-10	Sequence 10, Appl
20	3250.5	56.8	997	18	US-10-972-024-263	Sequence 263, App
21	3029.5	52.9	947	16	US-10-478-758-4	Sequence 4, Appli
22	2933	51.2	949	17	US-10-924-081-9	Sequence 9, Appli
23	2306	40.3	497	15	US-10-334-143-23	Sequence 23, Appl
24	1792.5	31.3	350	17	US-10-902-531-18	Sequence 18, Appl
25	1695	29.6	323	17	US-10-902-531-17	Sequence 17, Appl
26	1598	27.9	304	17	US-10-902-531-16	Sequence 16, Appl
27	1410	24.6	2172	20	US-11-097-143-30666	Sequence 30666, A
28	1322.5	23.1	1022	20	US-11-097-143-13494	Sequence 13494, A
29	1291	22.5	1191	20	US-11-097-143-9117	Sequence 9117, Ap
30	1189	20.8	1098	18	US-10-823-432-35	Sequence 35, Appl
31	1188	20.7	1150	17	US-10-924-081-3	Sequence 3, Appli
32	1184.5	20.7	1157	17	US-10-924-081-11	Sequence 11, Appl
33	1183.5	20.7	1076	14	US-10-116-949-6	Sequence 6, Appli
34	1183.5	20.7	1145	14	US-10-116-949-2	Sequence 2, Appli
35	1183.5	20.7	1145	14	US-10-116-949-4	Sequence 4, Appli
36	1183.5	20.7	1145	16	US-10-723-860-1799	Sequence 1799, Ap
37	1183.5	20.7	1145	17	US-10-482-029-114	Sequence 114, App
38	1183.5	20.7	1145	17	US-10-902-531-20	Sequence 20, Appl
39	1182.5	20.7	1157	17	US-10-924-081-1	Sequence 1, Appli
40	1182.5	20.7	1157	18	US-10-823-432-33	Sequence 33, Appl
41	1182.5	20.7	1157	18	US-10-823-432-34	Sequence 34, Appl
42	1182	20.6	1156	18	US-10-823-432-32	Sequence 32, Appl
43	1180	20.6	1148	18	US-10-823-432-36	Sequence 36, Appl
44	1179.5	20.6	1109	17	US-10-902-531-6	Sequence 6, Appli
45	1179.5	20.6	1115	17	US-10-902-531-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-833-222A-10
; Sequence 10, Application US/09833222A
; Publication No. US20030166045A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; TITLE OF INVENTION: cDNA encoding the Calcium Channel Alpha2Delta-4 Subunit
; FILE REFERENCE: calcium channel alpha2delta-4 subunit
; CURRENT APPLICATION NUMBER: US/09/833,222A
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1090
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-222A-10

Query Match 100.0%; Score 5726; DB 10; Length 1090;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAVALGTRRRDRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVR 60
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Db          1 MAVALGTRRRDRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVR 60

Qy         61 KFSEDMENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELG 120
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Db         61 KFSEDMENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELG 120

Qy        121 AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTL 180
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Qy        181 TWQYFGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKG 240
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Db        181 TWQYFGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKG 240

Qy        241 LRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEE 300

Qy        301 LMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCK 360

Qy        361 VRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHD 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHD 420

Qy        421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLA 480
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Db        421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLA 480

Qy        481 PRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLR 540
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Db        481 PRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLR 540

Qy        541 TAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGN 600
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Db        541 TAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGN 600

Qy        601 TSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVR 660
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Db        601 TSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVR 660

Qy        661 EVLFDAVVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFL 720
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Db        661 EVLFDAVVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFL 720

Qy        721 TPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDK 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDK 780

Qy        781 RTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKR 840
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Db        781 RTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKR 840

Qy        841 SRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTA 900
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Db        841 SRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTA 900

Qy        901 TRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAI 960
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Db        901 TRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAI 960

Qy        961 REANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDR 1020
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Db        961 REANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDR 1020

Qy       1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRQEHIGMPMNTPVPVL 1080
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Db       1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRQEHIGMPMNTPVPVL 1080

Qy       1081 LGGNIRVYAL 1090
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Db       1081 LGGNIRVYAL 1090
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RESULT 2
US-10-119-624-10
; Sequence 10, Application US/10119624
; Publication No. US20030170785A1
; GENERAL INFORMATION:
;  APPLICANT: Qin, Ning
;  APPLICANT:  Codd, Ellen
;  TITLE OF INVENTION: cDNA Encoding a Human No. US20030170785A1el Alpha2 Delta4 Calcium
;  FILE REFERENCE: ORT-1622
;  CURRENT APPLICATION NUMBER: US/10/119,624
;  CURRENT FILING DATE:  2002-04-10
;  PRIOR APPLICATION NUMBER: US 09/833,222
;  PRIOR FILING DATE: 2001-04-11
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 1090
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-119-624-10

  Query Match            100.0%;  Score 5726;  DB 14;  Length 1090;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1090;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAVALGTRRRDRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVR 60
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Db          1 MAVALGTRRRDRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVR 60

Qy         61 KFSEDMENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KFSEDMENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELG 120

Qy        121 AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTL 180
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Db        121 AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTL 180

Qy        181 TWQYFGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKG 240
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Db        181 TWQYFGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKG 240

Qy        241 LRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEE 300

Qy        301 LMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCK 360
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Db        301 LMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCK 360

Qy        361 VRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHD 420
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Db        361 VRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHD 420

Qy        421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLA 480
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Db        421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLA 480

Qy        481 PRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLR 540
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Db        481 PRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLR 540

Qy        541 TAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGN 600
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Db        541 TAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGN 600

Qy        601 TSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVR 660
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Db        601 TSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVR 660

Qy        661 EVLFDAVVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFL 720
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Db        661 EVLFDAVVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFL 720

Qy        721 TPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDK 780
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Db        721 TPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDK 780

Qy        781 RTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKR 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 RTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKR 840
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Qy        841 SRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTA 900
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Db        841 SRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTA 900

Qy        901 TRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAI 960
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Db        901 TRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAI 960

Qy        961 REANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDR 1020
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Db        961 REANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDR 1020

Qy       1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRQEHIGMPMNTPVPVL 1080
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Db       1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRQEHIGMPMNTPVPVL 1080

Qy       1081 LGGNIRVYAL 1090
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Db       1081 LGGNIRVYAL 1090
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RESULT 3
US-10-128-558-176
; Sequence 176, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 812A
; CURRENT APPLICATION NUMBER: US/10/128,558
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 176
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-558-176

Query Match 94.1%; Score 5385.5; DB 16; Length 1207;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1032; Conservative 6; Mismatches 13; Indels 3; Gaps 2;

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Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
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Db        145 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 204

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
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Db        205 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 264

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
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Db        265 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 324

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 384

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 TTILDTLGENDFINIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 444

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
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Db        445 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 504

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
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Db        505 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 564

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 624

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
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Db        625 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 684

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        685 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 744

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 804

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 864

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 924

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        925 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 984

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 1044

Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1045 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 1104

Qy        971 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1164

Qy       1031 DSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
              |||||||||   : | | |  :| :|  | | :|
Db       1165 DSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1197
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RESULT 4
US-10-257-174-34
; Sequence 34, Application US/10257174

```
; Publication No. US20040034194A1
; GENERAL INFORMATION:
;  APPLICANT: Agarwal, Pankaj
;  APPLICANT:  Murdoch, Paul R.
;  APPLICANT:  Rizvi, Safia K.
;  APPLICANT:  Smith, Randall F.
;  APPLICANT:  Xiang, Zhaoying
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP50022
;  CURRENT APPLICATION NUMBER: US/10/257,174
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: PCT/US01/11797
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: 60/196,603
;  PRIOR FILING DATE: 2000-04-13
;  PRIOR APPLICATION NUMBER: 60/199,417
;  PRIOR FILING DATE: 2000-04-24
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
;   LENGTH: 1075
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-257-174-34

  Query Match             91.4%;  Score 5234.5;  DB 15;  Length 1075;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 1011;  Conservative    7;  Mismatches   25;  Indels   11;  Gaps    4;

Qy         12 RVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLR 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 RVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLR 79

Qy         72 RKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHF 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 RKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHF 139

Qy        132 SNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGF 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGF 199

Qy        192 FRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTIT 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTIT 259

Qy        252 TILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQ 311
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 TILDTLGENDFINIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQ 319

Qy        312 ALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGRE 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 ALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGRE 379

Qy        372 VSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSK 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 VSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSK 439

Qy        432 LLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYA 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 LLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYA 499

Qy        492 FLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTL 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 FLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTL 559

Qy        552 SMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLL 611
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        560 SMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDLL 619

Qy        612 HPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAP 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 HPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAP 679

Qy        672 MEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTL 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 MEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTL 739

Qy        732 DRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQ 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 DRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQ 799

Qy        792 MKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEV 851
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        800 MKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEV 859

Qy        852 DGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLF 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 DGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLF 919

Qy        912 LLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECGP 971
              ||||||||||||||||        ||||||||||||||||||||||||||||||||||||
Db        920 LLEWSVWGSWYDRGAEA-------HKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECGP 972

Qy        972 CQKVFVVQQIPNSNLLLLVTDPT-CDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1030
              |||||||||||||||||||||| |     | :|       :||||||||||||||||||
Db        973 CQKVFVVQQIPNSNLLLLVTDPTFCRMGSGPEILTLTVASAHNASVKCDRMRSQKLRRRP 1032

Qy       1031 DSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
              |||||||||   : | | |  :| :|  | | :|
Db       1033 DSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1065


RESULT 5
US-10-257-174-35
; Sequence 35, Application US/10257174
; Publication No. US20040034194A1
; GENERAL INFORMATION:
;  APPLICANT: Agarwal, Pankaj
;  APPLICANT:  Murdoch, Paul R.
;  APPLICANT:  Rizvi, Safia K.
;  APPLICANT:  Smith, Randall F.
;  APPLICANT:  Xiang, Zhaoying
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP50022
;  CURRENT APPLICATION NUMBER: US/10/257,174
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: PCT/US01/11797
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: 60/196,603
;  PRIOR FILING DATE: 2000-04-13
;  PRIOR APPLICATION NUMBER: 60/199,417
;  PRIOR FILING DATE: 2000-04-24
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
;   LENGTH: 1114
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-257-174-35

  Query Match             91.3%;  Score 5230.5;  DB 15;  Length 1114;
  Best Local Similarity   95.7%;  Pred. No. 0;
  Matches 1010;  Conservative    8;  Mismatches   26;  Indels   11;  Gaps    4;

Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237
```

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Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTILDTLGENDFINIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 777

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 837

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        838 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 897

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 957

Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
              ||||||||||||||||        ||||||||||||||||||||||||||||||||||||
Db        958 FLLEWSVWGSWYDRGAEA-------HKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 1010

Qy        971 PCQKVFVVQQIPNSNLLLLVTDPT-CDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRR 1029
              |||||||||||||||||||||||| |      | :|       :||||||||||||||||||
Db       1011 PCQKVFVVQQIPNSNLLLLVTDPTFCRMGSGPEILTLTVASAHNASVKCDRMRSQKLRRR 1070

Qy       1030 PDSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
              ||||||||||   : | | |  :| :|  | | :|
Db       1071 PDSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1104
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RESULT 6
US-10-257-022-12
; Sequence 12, Application US/10257022
; Publication No. US20030211499A1
; GENERAL INFORMATION:
; APPLICANT: REDDY, Roopa
; APPLICANT: THORNTON, Michael
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: YAO, Monique G.
; APPLICANT: SANJANWALA, Madhusudan M.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: NGUYEN, Danniel B.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: YUE, Henry
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: LU, Yan
; APPLICANT: GREENE, Barrie D.
; APPLICANT: RAUMANN, Brigitte E.
; APPLICANT: Arvizu, Chandra S.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0067 USN
; CURRENT APPLICATION NUMBER: US/10/257,022
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US01/11206
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,595
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/196,872
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/199,020
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/200,552
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/202,348
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/203,495
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 1310
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7473443CD1
US-10-257-022-12

Query Match 66.5%; Score 3808; DB 15; Length 1310;
Best Local Similarity 80.5%; Pred. No. 4.3e-300;
Matches 750; Conservative 4; Mismatches 14; Indels 164; Gaps 2;

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Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 433

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLV---------------------------------- 98
              ||||||||||||||||||||||||||||
Db        434 RRKVEAVQNLVEAAEEADLNHEFNESLVEPGVGVGVGMSVTQSGVGVGVGMSVTQSGVGV 493

Qy         99 ---------------------------------------------------------- 98

Db        494 GVGMSITLSGVGVGVGMSVRQSGVGVGVGMSVTQSGVGVGVGMSVTQSGVGVGVGMSVRQ 553

Qy         99 ---------------------------------------------------------- 98

Db        554 SGVGVGVGMSVTQSWGVFSAQRAAAGACVDSDGRPAPALSSSHLRRFSSSLSACPGARAA 613

Qy         99 ---------FDYYNSVLINERDEKGNFVELGAEFLLESNAHFSNLPVNTSISSVQLPTNV 149
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 SVGLTRPPQFDYYNSVLINERDEKGNFVELGAEFLLESNAHFSNLPVNTSISSVQLPTNV 673

Qy        150 YNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFFRIYPGIKWTPDENGVIT 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 YNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFFRIYPGIKWTPDENGVIT 733
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Qy        210 FDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYN 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 FDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFINIIAYN 793

Qy        270 DYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQG 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 DYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQG 853

Qy        330 SLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREVSFADRMKWIACNNKGYY 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 SLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREVSFADRMKWIACNNKGYY 913

Qy        390 TQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKLLSSQAQSLTLLTTVAMP 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 TQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKLLSSQAQSLTLLTTVAMP 973

Qy        450 VFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPL 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 VFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPL 1033

Qy        510 YREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLSMDVKVPMDKGKRVLFLT 569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 YREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLSMDVKVPMDKGKRVLFLT 1093

Qy        570 NDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLLHPDLALAGDWIYCITDID 629
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 NDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDLLHPDLALAGDWIYCITDID 1153

Qy        630 PDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAPMEAYWTALALNMSEESEH 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1154 PDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAPMEAYWTALALNMSEESEH 1213

Qy        690 VVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAGSF 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1214 VVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAGSF 1273

Qy        750 VFNLRWAEGPESAGEPMVVTASTAVAVTVDKR 781
              |||||||||||   | |         :  |: ||
Db       1274 VFNLRWAEGP---GRPSAKGLPPPLCQTILKR 1302


RESULT 7
US-09-875-423-5
; Sequence 5, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
;  TITLE OF INVENTION:  FAMILY MEMBER AND USES THEREOF
;  FILE REFERENCE: 10448-059001
;  CURRENT APPLICATION NUMBER: US/09/875,423
;  CURRENT FILING DATE:  2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1091
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-875-423-5

  Query Match             59.8%;  Score 3422;  DB 9;  Length 1091;
  Best Local Similarity   60.0%;  Pred. No. 8.7e-269;
  Matches  627;  Conservative  188;  Mismatches  212;  Indels   18;  Gaps    6;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
              |||||  |||:: :   ||||| |||||||: |  : |||:|||:||:| :: || |  :
Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKIMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
              | |||: |||||||| | |||:  | ::|:|:|||||||: |||:||| ||:|  | ||:
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
              |||||  |:|  ||:|||:||||| |:|||| ||:|| |||:|| |||:| ||||||| |||
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
              | |||||| ||||||| |||||| ||||||||||:|||||||||||||||:|||| |:::
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
              |||||::|| ||| ||: :|||:|||  | |||||| |:|||:  :::|  ||:|::| |
Db        282 ILDTLGDDDFFNIITYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
              | ||| ||  |    |||:|:||||||:||||: |: :| |||||| |||:||||||||
Db        342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
              :||| :||:|| |||::|||||||| |||||||||||||| ||: :|||::|||||:|| |
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQA----QSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVH 488
              :|      | | |:|||||||||:||||| |||||||:|| ::||:|  |:||||:|
Db        462 PQAQKLADDQGLVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLGIH 521

Qy        489 GYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRET 548
              ||||  |||||||:||:|||| |||| : ||||:||||||||||: : || ||:||:|
Db        522 GYAFAITNNGYILTHPELRPLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNRKT 580

Qy        549 GTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLH 608
              |  ||:||  :||||||| :|||:::|||  ||||||  ||||||:|   || ::|||||
Db        581 GKFSMEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEGLH 640

Qy        609 DLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVV 668
              || |||:||  :|  || ||: |:|| ||||||:  :|  |:|  |:||:|||||::|||||||
Db        641 DLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVV 700

Qy        669 TAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASV 728
              :||:|||||:|||| || |:  |::|||||| || | :||||:|:::: ||   |: ::
Db        701 SAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENI 760

Qy        729 FTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAA 788
              |  | |||||||:|:|  |||||::: :: |  :  :  ||||||:: :  :::: : ||
Db        761 FNADHFPLWYRRAAEQIAGSFVYSIPFSTG--TVNKSNVVTASTSIQLLDERKSPVVAAV 818

Qy        789 GVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFL 848
              |:|||||| |||||  |:|||:::||  : ||:|  ::|::|||||||:|:   :|| |
Db        819 GIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFF 878

Qy        849 GEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQEL 908
              |||:|||: :||:|| | ::|:|||||||: :     :|  |: |  |||:| :|:: ||
Db        879 GEVEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDSAHGLLDPYKAFLSAAKWIMTEL 938

Qy        909 VLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVE 968
              ||||:|:::  ||:      ||:        | :  |:|||||| || :  |:|  | :
Db        939 VLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIA 990

Qy        969 CGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRR 1028
              |  | | ||:||||:||| ::| | :| |     |:     |::|| |:||:|:::||:||
Db        991 CEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKIRR 1050

Qy       1029 RPDSCHAFHPEVRVEADRGWAGFSS 1053
              ||:||| ||||   |  |   | ||
Db       1051 RPESCHGFHPE---ENARECGGASS 1072


RESULT 8
US-10-162-012-18
; Sequence 18, Application US/10162012
; Publication No. US20030051660A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
```

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;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,012
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,363
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 09/928,530
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: PCT/US01/25475
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: US 60/226,770
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 09/934,421
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: PCT/US01/26096
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 60/279,281
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 10/109,029
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: PCT/US02/09728
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/290,288
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 1091
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-162-012-18

  Query Match             59.8%;  Score 3422;  DB 14;  Length 1091;
  Best Local Similarity   60.0%;  Pred. No. 8.7e-269;
  Matches  627;  Conservative  188;  Mismatches  212;  Indels   18;  Gaps    6;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
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Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKIMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
              | |||: |||||||| | |||:  | ::|:|:|||||||: |||:||| ||:|  | ||:
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
              ||||| |:| ||:|||:||||| |:|||| ||:|| |||:|| |||:| |||||||| |||
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
              | |||||| ||||||| |||||| ||||||||||:|||||||||||||:|||| |:::
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
              ||||||::|| ||| ||: :||:|||  | |||||| |:|||:  :::|  ||:|::| |
Db        282 ILDTLGDDDFFNIITYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
              | ||| ||  |    |||:|:||||||:||||: |: :| |||||| |||:||||||||
Db        342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
              :||| :||:|| |||::|||||||| ||||||||||||| ||: :||::|||||:|| |
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQA----QSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVH 488
                :|      | | |:|||||||||||:|||| |||||||:|| ::||:|  |:||||:|
Db        462 PQAQKLADDQGLVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLGIH 521

Qy        489 GYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRET 548
              ||||  |||||||:||:|||| |||| : ||||:|||||||||||: : || ||:||:|
Db        522 GYAFAITNNGYILTHPELRPLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNRKT 580

Qy        549 GTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLH 608
              |  ||:||  :|||||| :||||::||| |||||  |||||:|   || ::|||||
Db        581 GKFSMEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEGLH 640

Qy        609 DLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVV 668
              || |||::|| :| || ||: |:|| ||||||:  :|  |:| |:|:||::||||||||
Db        641 DLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVV 700

Qy        669 TAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASV 728
              :||:|||||:|||| || |:  |::|||||| || | :||||:|:::::: ||    |: ::
Db        701 SAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENI 760

Qy        729 FTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAA 788
              |  | ||||||:|:|  |||||::: :: |  :  :  ||||||:: :  :::: : ||
Db        761 FNADHFPLWYRRAAEQIAGSFVYSIPFSTG--TVNKSNVVTASTSIQLLDERKSPVVAAV 818

Qy        789 GVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFL 848
              |:|||||| |||||  |:|||:::||  : ||:|  ::|::|||||||||:|:   :|| |
Db        819 GIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFF 878

Qy        849 GEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQEL 908
              |||:|||: :||:|| | ::|:|||||||: :     :|  |: |  |||:| :|:: ||
Db        879 GEVEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDSAHGLLDPYKAFLSAAKWIMTEL 938

Qy        909 VLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVE 968
              ||||:|:::  ||:      ||:         | :  |:|||||| || :  |:|  | :
Db        939 VLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIA 990

Qy        969 CGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRR 1028
              |  | | ||:||||:||| ::| | :| |    |:      |::|| |:||:|:::|:||
Db        991 CEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKIRR 1050

Qy       1029 RPDSCHAFHPEVRVEADRGWAGFSS 1053
              ||:||| ||||   |  |   | ||
Db       1051 RPESCHGFHPE---ENARECGGASS 1072


RESULT 9
US-10-162-102-18
; Sequence 18, Application US/10162102
; Publication No. US20030232336A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,102
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
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;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,363
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 1091
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-162-102-18

  Query Match             59.8%;  Score 3422;  DB 15;  Length 1091;
  Best Local Similarity   60.0%;  Pred. No. 8.7e-269;
  Matches  627;  Conservative  188;  Mismatches  212;  Indels   18;  Gaps    6;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
              |||||  |||:: :   ||||| |||||||: |  : |||:|||:||:| :: || |  :
Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKIMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
              | |||: |||||||| | |||:  | ::|:|:|||||||: |||:||| ||:|  | ||:
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
              ||||| |:| ||:|||:||||| |:|||| ||:|| |||:|| |||:| ||||||| |||
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
              | |||||| ||||||| |||||| ||||||||||:|||||||||||||:|||| |:::
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
              ||||||::|| ||| ||: :||:|||  | |||||| |:|||:  :::|  ||:|::| |
Db        282 ILDTLGDDDFFNIITYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
              | ||| ||  |    |||:|:|||||:||||: |: :| |||||| |||:||||||||
Db        342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
              :||| :||:|| |||::|||||||| |||||||||||||| ||: :||::|||||:|| |
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQA----QSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVH 488
                :|      | | |:|||||||||:|||| |||||||:|| ::||:|  |:||||:|
Db        462 PQAQKLADDQGLVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLGIH 521

Qy        489 GYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRET 548
              ||||  ||||||:||:||||| |||| : ||||:|||||||||: : || ||:||:|
Db        522 GYAFAITNNGYILTHPELRPLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNRKT 580

Qy        549 GTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLH 608
              |  ||:||  :||||||| :||||::|||  ||||||  ||||||:|   || ::|||||
Db        581 GKFSMEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEGLH 640

Qy        609 DLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVV 668
              || |||::|| :| || ||: |:|| ||||||:  :|  |:| |:||:||::||||||||
Db        641 DLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVV 700

Qy        669 TAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASV 728
              :||:|||||:|||| || |:  |::|||||| || | :||||:|:::::: ||   |: ::
Db        701 SAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENI 760

Qy        729 FTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAA 788
              |  | ||||||:|:|  |||||::: :: |  :  :  ||||||:: :  :::: : ||
Db        761 FNADHFPLWYRRAAEQIAGSFVYSIPFSTG--TVNKSNVVTASTSIQLLDERKSPVVAAV 818

Qy        789 GVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFL 848
              |:|||||| ||||| |:|||:::||  : ||:|  ::|::|||||||||:|:   :|| |
Db        819 GIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFF 878

Qy        849 GEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQEL 908
              |||:|||: :||:|| | ::|:|||||||: :     :|  |: |  |||:| :|:: ||
Db        879 GEVEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDSAHGLLDPYKAFLSAAKWIMTEL 938

Qy        909 VLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVE 968
              ||||:|:::  ||:      ||:          | :  |:|||||| || :  |:|  | :
Db        939 VLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIA 990

Qy        969 CGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRR 1028
              |  | | ||:||||:||| ::| | :| |    |:     |::|| |:||:|:::||:||
Db        991 CEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKIRR 1050

Qy       1029 RPDSCHAFHPEVRVEADRGWAGFSS 1053
              ||:||| ||||   |  |   | ||
Db       1051 RPESCHGFHPE---ENARECGGASS 1072


RESULT 10
US-10-902-531-24
; Sequence 24, Application US/10902531
; Publication No. US20050042659A1
; GENERAL INFORMATION:
;  APPLICANT: Warner-Lambert
;  TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE: 180
;  CURRENT APPLICATION NUMBER: US/10/902,531
;  CURRENT FILING DATE:  2004-07-29
;  PRIOR APPLICATION NUMBER: US/09/397,550
;  PRIOR FILING DATE: 1999-09-16
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 1077
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-902-531-24

  Query Match             59.7%;  Score 3419.5;  DB 17;  Length 1077;
  Best Local Similarity   60.3%;  Pred. No. 1.4e-268;
  Matches  622;  Conservative  188;  Mismatches  206;  Indels   15;  Gaps    5;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
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Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKIMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
              | |||: |||||||| | |||:  | ::|:|:|||||||: |||:||| ||:|  | ||:
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
              ||||| |:| ||:|||:||||| |:|||| ||:|| |||:|| |||:| ||||||| |||
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
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Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
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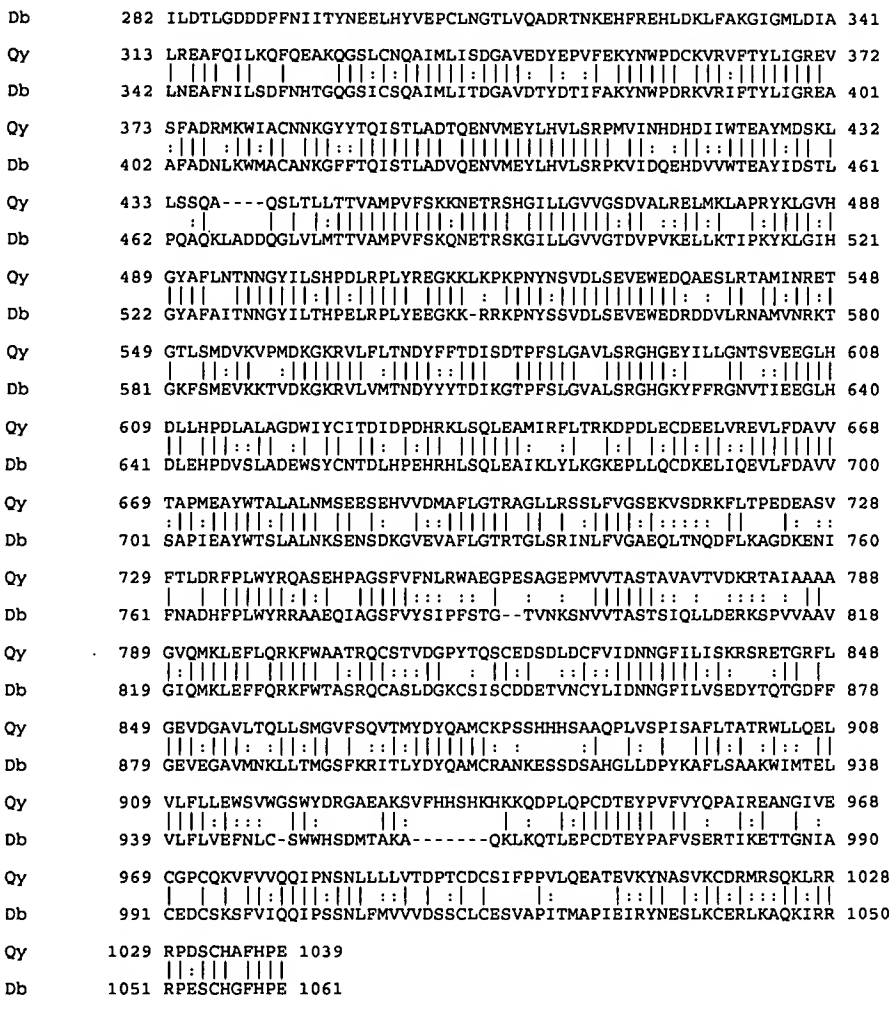
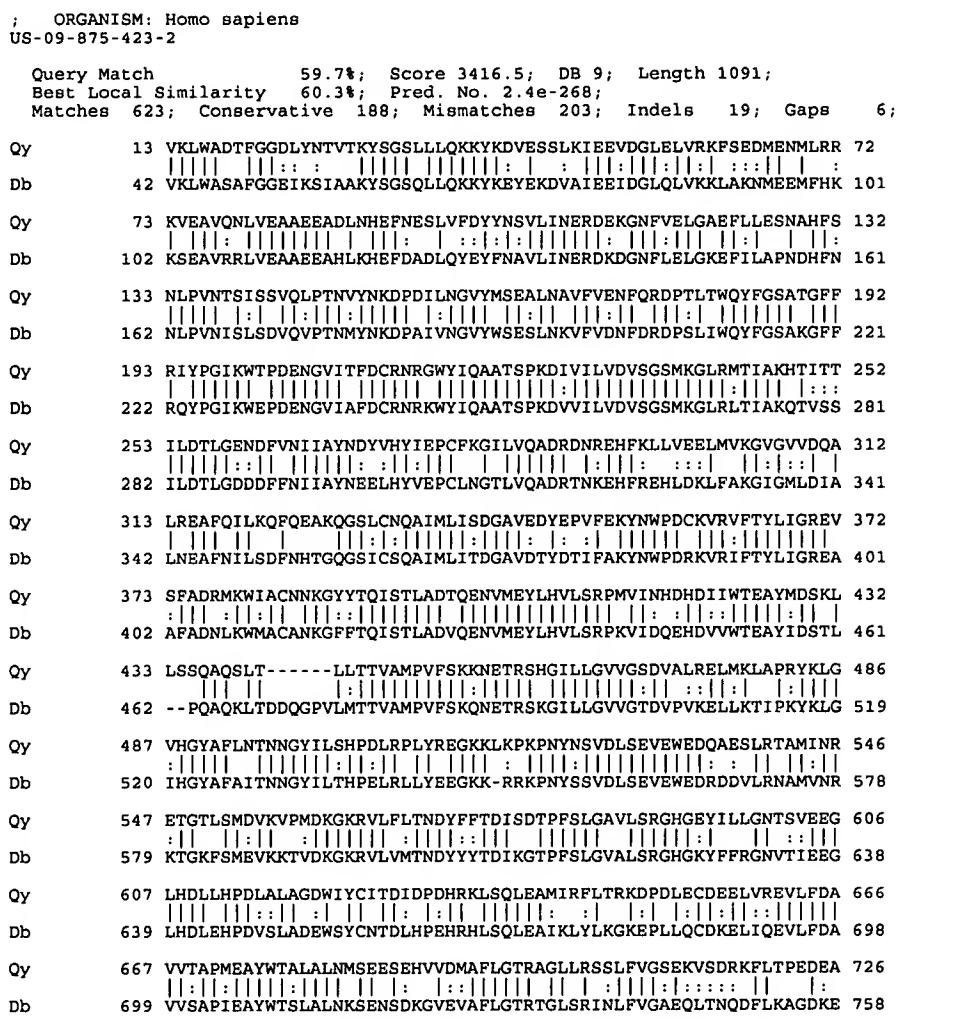


RESULT 11
US-09-875-423-2
; Sequence 2, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1091
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-875-423-2

Query Match 59.7%; Score 3416.5; DB 9; Length 1091;
Best Local Similarity 60.3%; Pred. No. 2.4e-268;
Matches 623; Conservative 188; Mismatches 203; Indels 19; Gaps 6;



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Db        989 IACEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKI 1048

Qy       1027 RRRPDSCHAFHPE 1039
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Db       1049 RRRPESCHGFHPE 1061


RESULT 12
US-10-162-012-15
; Sequence 15, Application US/10162012
; Publication No. US20030051660A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,012
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,363
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 09/928,530
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: PCT/US01/25475
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: US 60/226,770
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 09/934,421
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: PCT/US01/26096
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 60/279,281
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 10/109,029
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: PCT/US02/09728
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/290,288
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 1091
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-162-012-15

  Query Match             59.7%;  Score 3416.5;  DB 14;  Length 1091;
  Best Local Similarity   60.3%;  Pred. No. 2.4e-268;
  Matches  623;  Conservative  188;  Mismatches  203;  Indels   19;  Gaps    6;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
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Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKNMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
              | |||: |||||||| | |||:  | ::|:|:|||||||: |||:||| ||:|  | ||:
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
              ||||| |:| ||:|||:||||| |:|||| ||:|| |||:|| ||||:| ||||||| |||
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
              | |||||| ||||||| |||||| ||||||||||:|||||||||||||:|||| |:::
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
              ||||||::|| |||||: :||:|||  | |||||| |:|||:  :::|  ||:|::| |
Db        282 ILDTLGDDDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
              | ||| ||  |    |||:|:||||||:|||: |: :| |||||| |||:||||||||
Db        342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
              :||| :||:|| |||::|||||||| |||||||||||||| ||: :||::|||||:|| |
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQAQSLT------LLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLG 486
                 ||| ||      |:|||||||||:||||| ||||||||:|| ::||:|  |:||||
Db        462 --PQAQKLTDDQGPVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLG 519

Qy        487 VHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINR 546
              :|||||  |||||||:||:|| || |||| : ||||:|||||||||||: : || ||:||
Db        520 IHGYAFAITNNGYILTHPELRLLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNR 578

Qy        547 ETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEG 606
              :||  ||:||  :||||||| :||||::|||  ||||||  ||||||:|   || ::|||
Db        579 KTGKFSMEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEG 638

Qy        607 LHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDA 666
              |||| |||::|| :| || ||: |:|| ||||||:  :|  |:| |:||:||::||||||
Db        639 LHDLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDA 698

Qy        667 VVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEA 726
              ||:||:|||||:|||| || |:  |::|||||| || | :||||:|::::: ||   |:
Db        699 VVSAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKE 758

Qy        727 SVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAA 786
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Db        759 NIFNADHFPLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVVA 816

Qy        787 AAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGR 846
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Db        817 AVGIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGD 876

Qy        847 FLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQ 906
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Db        877 FFGEIEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPYNAFLSAVKWIMT 936

Qy        907 ELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGI 966
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Db        937 ELVLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGN 988

Qy        967 VECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKL 1026
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Db        989 IACEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKI 1048

Qy       1027 RRRPDSCHAFHPE 1039
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Db       1049 RRRPESCHGFHPE 1061


RESULT 13
US-10-162-102-15
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; Sequence 15, Application US/10162102
; Publication No. US20030232336A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,102
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,363
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 1091
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-162-102-15

  Query Match             59.7%;  Score 3416.5;  DB 15;  Length 1091;
  Best Local Similarity   60.3%;  Pred. No. 2.4e-268;
  Matches  623;  Conservative  188;  Mismatches  203;  Indels   19;  Gaps    6;

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Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
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Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
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Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
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Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQAQSLT------LLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLG 486
Db        462 --PQAQKLTDDQGPVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLG 519

Qy        487 VHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINR 546
Db        520 IHGYAFAITNNGYILTHPELRLLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNR 578

Qy        547 ETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPPSLGAVLSRGHGEYILLGNTSVEEG 606
Db        579 KTGKFSMEVKKTVDKGKRVLVMTNDYYYTDIKGTPPSLGVALSRGHGKYFFRGNVTIEEG 638

Qy        607 LHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDA 666
Db        639 LHDLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDA 698

Qy        667 VVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEA 726
Db        699 VVSAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKE 758

Qy        727 SVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAA 786
Db        759 NIFNADHFPLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVVA 816

Qy        787 AAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGR 846
Db        817 AVGIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGD 876

Qy        847 FLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQ 906
Db        877 FFGEIEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPYNAFLSAVKWIMT 936

Qy        907 ELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGI 966
Db        937 ELVLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGN 988

Qy        967 VECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKL 1026
Db        989 IACEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKI 1048

Qy       1027 RRRPDSCHAFHPE 1039
Db       1049 RRRPESCHGFHPE 1061


RESULT 14
US-10-924-081-6
; Sequence 6, Application US/10924081
; Publication No. US20050095678A1
; GENERAL INFORMATION:
;  APPLICANT: PARKER, David
;  APPLICANT:  XU, Xianghong
;  APPLICANT:  KHAWAJA, Afsheen
;  APPLICANT:  SNUTCH, Terrance P.
;  TITLE OF INVENTION: NOVEL RAT CALCIUM CHANNEL SUBUNITS AND
;  TITLE OF INVENTION:  RELATED PROBES, CELL LINES AND METHODS
;  FILE REFERENCE: 381092001400
;  CURRENT APPLICATION NUMBER: US/10/924,081
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: PCT/CA2004/001550
;  PRIOR FILING DATE: 2004-08-23
;  PRIOR APPLICATION NUMBER: US 60/497,096
;  PRIOR FILING DATE: 2003-08-22
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 1091
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-924-081-6

  Query Match             59.6%;  Score 3411;  DB 17;  Length 1091;
  Best Local Similarity   59.6%;  Pred. No. 6.8e-268;
  Matches  623;  Conservative  191;  Mismatches  213;  Indels   18;  Gaps    6;
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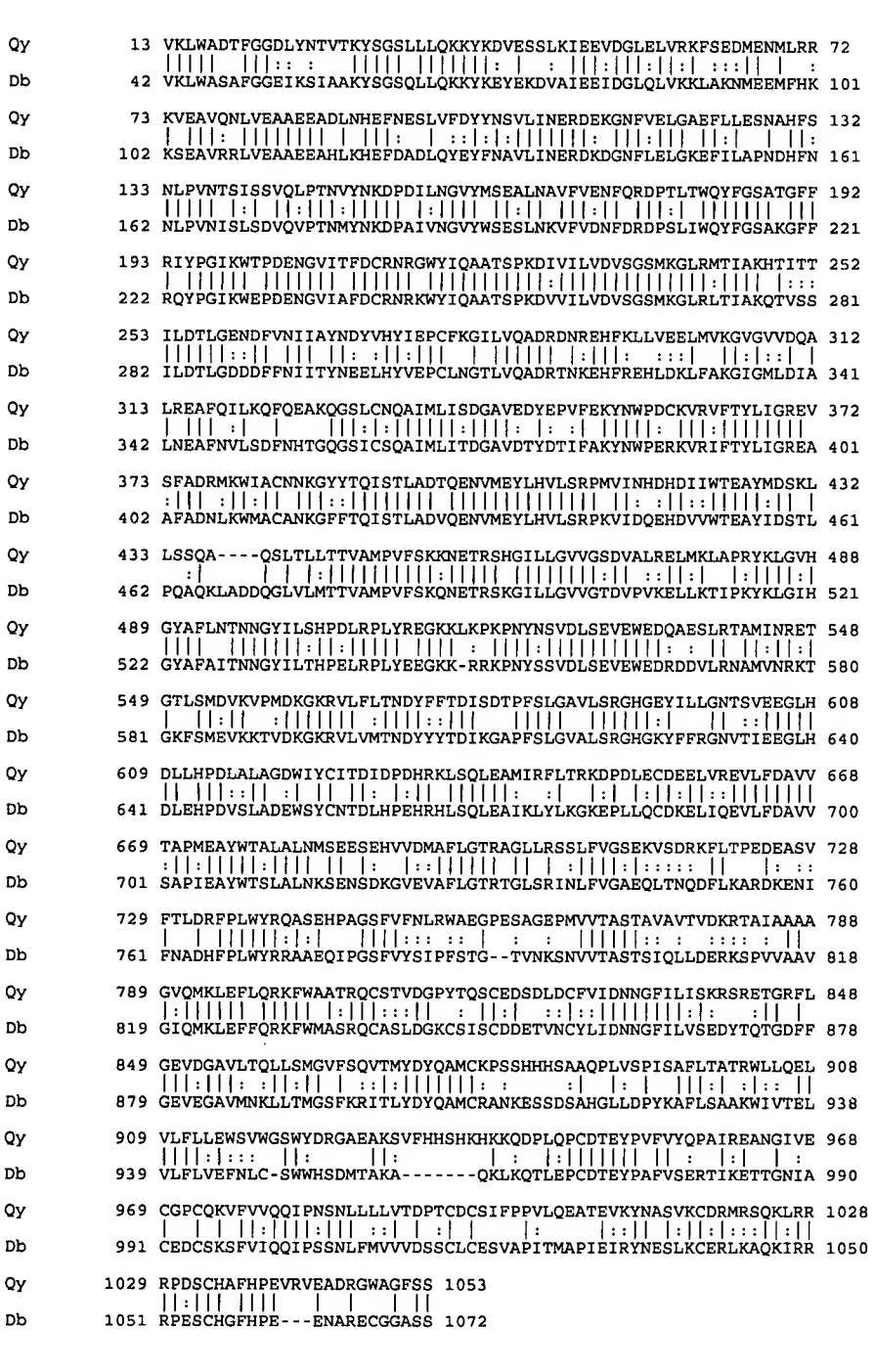

RESULT 15
US-10-902-531-12
; Sequence 12, Application US/10902531
; Publication No. US20050042659A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/10/902,531
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/397,550
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1065
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-902-531-12

Query Match 59.6%; Score 3410.5; DB 17; Length 1065;
Best Local Similarity 60.3%; Pred. No. 7.2e-268;
Matches 619; Conservative 188; Mismatches 207; Indels 13; Gaps 5;

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Db        759 HFPLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVVAAVGIQM 816

Qy        793 KLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEVD 852
              |||| ||||| |:|||:::|| : ||:|  ::|::|||||||:|:   :|| | ||::
Db        817 KLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFFGEIE 876

Qy        853 GAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFL 912
              |||: :||:|| | ::|:|||||||: :      |  |: | :|||:| :|:: ||||||
Db        877 GAVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPYNAFLSAVKWIMTELVLFL 936

Qy        913 LEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECGPC 972
              :|:::  ||:     ||:       | :  |:|||||| || :  |:|  | : |  |
Db        937 VEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIACEDC 988

Qy        973 QKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRPDS 1032
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Qy       1033 CHAFHPE 1039
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Search completed: November 16, 2005, 03:37:42
Job time : 180 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 17, 2005, 03:21:06 ; Search time 1916 Seconds
(without alignments)
4704.647 Million cell updates/sec

Title: US-09-833-222A-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTPVPVLLGGNIRVYAL 1090

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5726	100.0	3486	10	US-09-833-222A-9	Sequence 9, Appli
2	5726	100.0	3486	17	US-10-119-624-9	Sequence 9, Appli
3	5385.5	94.1	4841	21	US-10-128-558-52	Sequence 52, Appl
4	5234.5	91.4	3228	19	US-10-257-174-10	Sequence 10, Appl
5	5230.5	91.3	3345	19	US-10-257-174-11	Sequence 11, Appl
6	3808	66.5	4125	18	US-10-257-022-27	Sequence 27, Appl
7	3422.5	59.8	3598	22	US-10-924-081-5	Sequence 5, Appli
8	3421.5	59.8	3528	9	US-09-728-628-12	Sequence 12, Appl
9	3421.5	59.8	3528	24	US-10-972-024-117	Sequence 117, App
10	3416.5	59.7	3276	9	US-09-875-423-3	Sequence 3, Appli
11	3416.5	59.7	3276	15	US-10-162-012-16	Sequence 16, Appl
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14	3416.5	59.7	3690	15	US-10-162-012-14	Sequence 14, Appl
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16	3410.5	59.6	3770	22	US-10-902-531-21	Sequence 21, Appl
17	3400.5	59.4	3213	22	US-10-902-531-9	Sequence 9, Appli
18	3326.5	58.1	3114	22	US-10-902-531-8	Sequence 8, Appli
19	3278.5	57.3	3057	22	US-10-902-531-7	Sequence 7, Appli
20	3195.5	55.8	3382	20	US-10-478-758-13	Sequence 13, Appl
21	2944.5	51.4	3172	22	US-10-924-081-8	Sequence 8, Appli
22	2306	40.3	1523	18	US-10-334-143-107	Sequence 107, App
23	1792.5	31.3	1050	22	US-10-902-531-15	Sequence 15, Appl
24	1695	29.6	969	22	US-10-902-531-14	Sequence 14, Appl
25	1598	27.9	912	22	US-10-902-531-13	Sequence 13, Appl
26	1410	24.6	6519	26	US-11-097-143-30665	Sequence 30665, A
27	1362.5	23.8	856	19	US-10-220-120-103	Sequence 103, App
28	1336.5	23.3	3414	26	US-11-097-143-13493	Sequence 13493, A
29	1329	23.2	13293	26	US-11-097-143-30664	Sequence 30664, A
30	1291	22.5	3576	26	US-11-097-143-9116	Sequence 9116, Ap
31	1192	20.8	5733	21	US-10-417-375-171	Sequence 171, App
32	1188.5	20.8	5279	15	US-10-116-949-5	Sequence 5, Appli
33	1188	20.7	4993	22	US-10-924-081-2	Sequence 2, Appli
34	1187.5	20.7	5303	21	US-10-723-860-1798	Sequence 1798, Ap
35	1187.5	20.7	5463	15	US-10-116-949-1	Sequence 1, Appli
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39	1187.5	20.7	5730	21	US-10-417-375-173	Sequence 173, App
40	1184.5	20.7	3474	22	US-10-924-081-10	Sequence 10, Appl
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43	1178.5	20.6	4182	21	US-10-417-375-175	Sequence 175, App
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ALIGNMENTS

RESULT 1
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; Sequence 9, Application US/09833222A
; Publication No. US20030166045A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; TITLE OF INVENTION: cDNA encoding the Calcium Channel Alpha2Delta-4 Subunit
; FILE REFERENCE: calcium channel alpha2delta-4 subunit
; CURRENT APPLICATION NUMBER: US/09/833,222A
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9

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;   LENGTH: 3486
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-833-222A-9

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Best Local Similarity:  100.00%     Mismatches:     0
Query Match:            100.00%     Indels:         0
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Qy         81 ValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGluSerLeuValPheAsp 100
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Qy        601 ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAsp 620
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Db      2350 ACACCTGAGGACGAGGCCAGCGTGTTCACCCTGGACCGCTTCCCGCTGTGGTACCGCCAG 2409

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Db      2410 GCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCTCCGCTGGGCAGAAGGACCAGAA 2469

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Qy       941 GlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAlaIle 960
Db      3010 CAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCCATC 3069

Qy       961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGlnGln 980
Db      3070 CGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAG 3129

Qy       981 IleProAsnSerAsnLeuLeuLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
Db      3130 ATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATCTTC 3189

Qy      1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
Db      3190 CCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGCCTCTGTCAAATGTGACCGG 3249

Qy      1021 MetArgSerGlnLysLeuArgArgArgProAspSerCysHisAlaPheHisProGluVal 1040
Db      3250 ATGCGCTCCCAGAAGCTCCGCCGGCGACCAGACTCCTGCCACGCCTTCCATCCAGAGGTG 3309

Qy      1041 ArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGly 1060
Db      3310 CGGGTTGAGGCGGATCGAGGGTGGGCTGGATTTTCATCCCCAAACCCTCTGTGCCTGGGT 3369

Qy      1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
Db      3370 CTGTGCCCCTGCAGACAGGAGCATATAGGGATGCCAATGAACACACCTGTGCCTGTGCTT 3429

Qy      1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
Db      3430 CTCGGGGGAAACATTCGCGTTTATGCCCTG 3459
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RESULT 2
US-10-119-624-9
; Sequence 9, Application US/10119624
; Publication No. US20030170785A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; TITLE OF INVENTION: cDNA Encoding a Human No. US20030170785A1el Alpha2 Delta4 Calcium
; FILE REFERENCE: ORT-1622
; CURRENT APPLICATION NUMBER: US/10/119,624
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 09/833,222
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-119-624-9

Alignment Scores:

Pred. No.:	0	Length:	3486
Score:	5726.00	Matches:	1090
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-09-833-222A-10 (1-1090) x US-10-119-624-9 (1-3486)

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Qy         1 MetAlaValAlaLeuGlyThrArgArgArgAspArgValLysLeuTrpAlaAspThrPhe 20
Db       190 ATGGCTGTAGCTTTAGGGACAAGGAGGAGGGACAGAGTGAAGCTATGGGCTGACACCTTC 249

Qy        21 GlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeuLeuLeuGlnLysLys 40
Db       250 GGCGGGGACCTGTATAACACTGTGACCAAATACTCAGGCTCTCTCTTGCTGCAGAAGAAG 309

Qy        41 TyrLysAspValGluSerSerLeuLysIleGluGluValAspGlyLeuGluLeuValArg 60
Db       310 TACAAGGATGTGGAGTCCAGTCTGAAGATCGAGGAGGTGGATGGCTTGGAGCTGGTGAGG 369

Qy        61 LysPheSerGluAspMetGluAsnMetLeuArgArgLysValGluAlaValGlnAsnLeu 80
Db       370 AAGTTCTCAGAGGACATGGAGAACATGCTGCGGAGGAAAGTCGAGGCGGTCCAGAATCTG 429

Qy        81 ValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGluSerLeuValPheAsp 100
Db       430 GTGGAAGCTGCCGAGGAGGCCGACCTGAACCACGAATTCAATGAATCCCTGGTGTTCGAC 489

Qy       101 TyrTyrAsnSerValLeuIleAsnGluArgAspGluLysGlyAsnPheValGluLeuGly 120
Db       490 TATTACAACTCGGTCCTGATCAACGAGAGGGACGAGAAGGGCAACTTCGTGGAGCTGGGC 549

Qy       121 AlaGluPheLeuLeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIle 140
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Db        550 GCCGAGTTCCTCCTGGAGTCCAATGCTCACTTCAGCAACCTGCCGGTGAACACCTCCATC 609

Qy        141 SerSerValGlnLeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyVal 160

Db        610 AGCAGCGTGCAGCTGCCCACCAACGTGTACAACAAAGACCCAGATATTTTAAATGGAGTC 669

Qy        161 TyrMetSerGluAlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeu 180

Db        670 TACATGTCTGAAGCCTTGAATGCTGTCTTCGTGGAGAACTTCCAGAGAGACCCAACGTTG 729

Qy        181 ThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrp 200

Db        730 ACCTGGCAATATTTTGGCAGTGCAACTGGATTCTTCAGGATCTATCCAGGTATAAAATGG 789

Qy        201 ThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGln 220

Db        790 ACACCTGATGAGAATGGAGTCATTACTTTTGACTGCCGAAACCGCGGCTGGTACATTCAA 849

Qy        221 AlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMetLysGly 240

Db        850 GCTGCTACTTCTCCCAAGGACATAGTGATTTTGGTGGACGTGAGCGGCAGTATGAAGGGG 909

Qy        241 LeuArgMetThrIleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAsn 260

Db        910 CTGAGGATGACTATTGCCAAGCACACCATCACCACCATCTTGGACACCCTGGGGGAGAAT 969

Qy        261 AspPheValAsnIleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLys 280

Db        970 GACTTCGTTAATATCATAGCGTACAATGACTACGTCCATTACATCGAGCCTTGTTTTAAA 1029

Qy        281 GlyIleLeuValGlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuValGluGlu 300

Db       1030 GGGATCCTCGTCCAGGCGGACCGAGACAATCGAGAGCATTTCAAACTGCTGGTGGAGGAG 1089

Qy        301 LeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeu 320

Db       1090 TTGATGGTCAAAGGTGTGGGGGTCGTGGACCAAGCCCTGAGAGAAGCCTTCCAGATCCTG 1149

Qy        321 LysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSer 340

Db       1150 AAGCAGTTCCAAGAGGCCAAGCAAGGAAGCCTCTGCAACCAGGCCATCATGCTCATCAGC 1209

Qy        341 AspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLys 360

Db       1210 GACGGCGCCGTGGAGGACTACGAGCCGGTGTTTGAGAAGTATAACTGGCCAGACTGTAAG 1269

Qy        361 ValArgValPheThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrp 380

Db       1270 GTCCGAGTTTTCACTTACCTCATTGGGAGAGAAGTGTCTTTTGCTGACCGCATGAAGTGG 1329

Qy        381 IleAlaCysAsnAsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGlu 400

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Qy        401 AsnValMetGluTyrLeuHisValLeuSerArgProMetValIleAsnHisAspHisAsp 420

Db       1390 AACGTGATGGAATACCTGCACGTGCTCAGCCGCCCCATGGTCATCAACCACGACCACGAC 1449

Qy        421 IleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeu 440

Db       1450 ATCATCTGGACAGAGGCCTACATGGACAGCAAGCTCCTCAGCTCGCAGGCTCAGAGCCTG 1509

Qy        441 ThrLeuLeuThrThrValAlaMetProValPheSerLysLysAsnGluThrArgSerHis 460

Db       1510 ACACTGCTCACCACTGTGGCCATGCCAGTCTTCAGCAAGAAGAACGAAACGCGATCCCAT 1569

Qy        461 GlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAla 480

Db       1570 GGCATTCTCCTGGGTGTGGTGGGCTCAGATGTGGCCCTGAGAGAGCTGATGAAGCTGGCG 1629

Qy        481 ProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIle 500

Db       1630 CCCCGGTACAAGCTTGGAGTGCACGGATACGCCTTTCTGAACACCAACAATGGCTACATC 1689

Qy        501 LeuSerHisProAspLeuArgProLeuTyrArgGluGlyLysLysLeuLysProLysPro 520

Db       1690 CTCTCCCATCCCGACCTCCGGCCCCTGTACAGAGAGGGGAAGAAACTAAAACCCAAACCT 1749

Qy        521 AsnTyrAsnSerValAspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArg 540

Db       1750 AACTACAACAGTGTGGATCTCTCCGAAGTGGAGTGGGAAGACCAGGCTGAATCTCTGAGA 1809

Qy        541 ThrAlaMetIleAsnArgGluThrGlyThrLeuSerMetAspValLysValProMetAsp 560

Db       1810 ACAGCCATGATCAATAGGGAAACAGGTACTCTCTCGATGGATGTGAAGGTTCCGATGGAT 1869

Qy        561 LysGlyLysArgValLeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThr 580

Db       1870 AAAGGGAAGCGAGTTCTTTTCCTGACCAATGACTACTTCTTCACGGACATCAGCGACACC 1929

Qy        581 ProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsn 600

Db       1930 CCTTTCAGTTTGGGGGCGGTGCTGTCCCGGGGCCACGGAGAATACATCCTTCTGGGGAAC 1989

Qy        601 ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAsp 620

Db       1990 ACGTCTGTGGAAGAAGGCCTGCATGACTTGCTTCACCCAGACCTGGCCCTGGCCGGTGAC 2049

Qy        621 TrpIleTyrCysIleThrAspIleAspProAspHisArgLysLeuSerGlnLeuGluAla 640

Db       2050 TGGATCTACTGCATCACAGATATTGACCCAGACCACCGGAAGCTCAGCCAGCTAGAGGCC 2109

Qy        641 MetIleArgPheLeuThrArgLysAspProAspLeuGluCysAspGluGluLeuValArg 660

Db       2110 ATGATCCGCTTCCTCACCAGGAAGGACCCAGACCTGGAGTGTGACGAGGAGCTGGTCCGG 2169

Qy        661 GluValLeuPheAspAlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAla 680

Db       2170 GAGGTGCTGTTTGACGCGGTGGTGACAGCCCCCATGGAAGCCTACTGGACAGCGCTGGCC 2229

Qy        681 LeuAsnMetSerGluGluSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700

Db       2230 CTCAACATGTCCGAGGAGTCTGAACACGTGGTGGACATGGCCTTCCTGGGCACCCGGGCT 2289

Qy        701 GlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPheLeu 720

Db       2290 GGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGTCTCCGACAGGAAGTTCCTG 2349

Qy        721 ThrProGluAspGluAlaSerValPheThrLeuAspArgProProLeuTrpTyrArgGln 740

Db       2350 ACACCTGAGGACGAGGCCAGCGTGTTCACCCTGGACCGCTTCCCGCTGTGGTACCGCCAG 2409

Qy        741 AlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGlu 760

Db       2410 GCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCTCCGCTGGGCAGAAGGACCAGAA 2469

Qy        761 SerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLys 780

Db       2470 AGTGCGGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGTGGCGGTGACCGTGGACAAG 2529

Qy        781 ArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLys 800

Db       2530 AGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAA 2589

Qy        801 PheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGlu 820

Db       2590 TTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCCGTACACACAGAGCTGCGAG 2649

Qy        821 AspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArg 840

Db       2650 GACAGTGATCTGGACTGCTTCGTCATCGACAACAACGGGTTCATTCTGATCTCCAAGAGG 2709

Qy        841 SerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeu 860

Db       2710 TCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGCTGTCCTGACCCAGCTGCTC 2769
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Qy        861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2770 AGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCAGGCCATGTGCAAACCCTCG 2829

Qy        881 SerHisHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAla 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2830 AGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACGGCG 2889

Qy        901 ThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySer 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2890 ACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGCTCC 2949

Qy        921 TrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLysLys 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2950 TGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCACTCCCACAAACACAAGAAG 3009

Qy        941 GlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAlaIle 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 CAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCCATC 3069

Qy        961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGlnGln 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 CGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAG 3129

Qy        981 IleProAsnSerAsnLeuLeuLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 ATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATCTTC 3189

Qy       1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3190 CCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGCCTCTGTCAAATGTGACCGG 3249

Qy       1021 MetArgSerGlnLysLeuArgArgArgProAspSerCysHisAlaPheHisProGluVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 ATGCGCTCCCAGAAGCTCCGCCGGCGACCAGACTCCTGCCACGCCTTCCATCCAGAGGTG 3309

Qy       1041 ArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGly 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3310 CGGGTTGAGGCGGATCGAGGGTGGGCTGGATTTTCATCCCCAAACCCTCTGTGCCTGGGT 3369

Qy       1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3370 CTGTGCCCCTGCAGACAGGAGCATATAGGGATGCCAATGAACACACCTGTGCCTGTGCTT 3429

Qy       1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
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Db       3430 CTCGGGGGAAACATTCGCGTTTATGCCCTG 3459

RESULT 3
US-10-128-558-52
; Sequence 52, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Weng, Gezhi
;  APPLICANT:  Boyle, Bryan J
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 812A
;  CURRENT APPLICATION NUMBER: US/10/128,558
;  CURRENT FILING DATE:  2002-04-22
;  PRIOR APPLICATION NUMBER: US 60/339,453
;  PRIOR FILING DATE: 2001-12-11
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/35017
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/03800
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 412
;  SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 52
;    LENGTH: 4841
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (66)..(3689)
US-10-128-558-52

Alignment Scores:
Pred. No.:              0              Length:          4841
Score:                  5385.50        Matches:         1034
Percent Similarity:     97.47%         Conservative:    5
Best Local Similarity:  97.00%         Mismatches:      27
Query Match:            94.05%         Indels:          1
DB:                     21             Gaps:            0

US-09-833-222A-10 (1-1090) x US-10-128-558-52 (1-4841)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 557

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 617

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 677

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 737

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 797

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 857

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 917

Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 977

Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 1037

Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1038 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 1097

Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
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Db      1098 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 1157

Qy       231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250

Db      1158 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 1217

Qy       251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270

Db      1218 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCATTAATATCATAGCGTACAATGAC 1277

Qy       271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290

Db      1278 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1337

Qy       291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310

Db      1338 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1397

Qy       311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330

Db      1398 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1457

Qy       331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350

Db      1458 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1517

Qy       351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370

Db      1518 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1577

Qy       371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390

Db      1578 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1637

Qy       391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410

Db      1638 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1697

Qy       411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430

Db      1698 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1757

Qy       431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450

Db      1758 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1817

Qy       451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470

Db      1818 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1877

Qy       471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490

Db      1878 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1937

Qy       491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510

Db      1938 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1997

Qy       511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530

Db      1998 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 2057

Qy       531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550

Db      2058 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 2117

Qy       551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570

Db      2118 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 2177

Qy       571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590

Db      2178 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 2237

Qy       591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610

Db      2238 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 2297

Qy       611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630

Db      2298 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2357

Qy       631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650

Db      2358 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2417

Qy       651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670

Db      2418 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2477

Qy       671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690

Db      2478 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2537

Qy       691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710

Db      2538 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2597

Qy       711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730

Db      2598 TCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACC 2657

Qy       731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750

Db      2658 CTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTC 2717

Qy       751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770

Db      2718 TTCAACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCA 2777

Qy       771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyVal 790

Db      2778 AGCACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTC 2837

Qy       791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810

Db      2838 CAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACT 2897

Qy       811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830

Db      2898 GTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGAC 2957

Qy       831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850

Db      2958 AACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 3017

Qy       851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870

Db      3018 GTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATG 3077

Qy       871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890

Db      3078 TATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTG 3137

Qy       891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910

Db      3138 GTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTG 3197

Qy       911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930

Db      3198 TTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGT 3257

Qy       931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950

Db      3258 GTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAG 3317
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Qy        951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3318 TACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGG 3377

Qy        971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3378 CCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTG 3437

Qy        991 ThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3438 ACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGTC 3497

Qy       1011 LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgPro 1030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3498 AAATATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACCA 3557

Qy       1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGly 1050
              |||||||||||||||||||||||||  :::  |||  :::
Db       3558 GACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGCGGCGCCTCGGAC 3617

Qy       1051 PheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
              |||:::      ||||||  |||     |||  |||
Db       3618 ACCTCAGCCTCGCCGCCCCTACTCCTGCT-GCCTGTGTGTGCCTGGGGGCTACTGCCCCA 3676

Qy       1071 MetProMetAsnThrPro 1076
              |||      ||||||
Db       3677 ACTCCTGCGGTGACACCA 3694

RESULT 4
US-10-257-174-10
; Sequence 10, Application US/10257174
; Publication No. US20040034194A1
; GENERAL INFORMATION:
;  APPLICANT: Agarwal, Pankaj
;  APPLICANT:  Murdoch, Paul R.
;  APPLICANT:  Rizvi, Safia K.
;  APPLICANT:  Smith, Randall F.
;  APPLICANT:  Xiang, Zhaoying
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP50022
;  CURRENT APPLICATION NUMBER: US/10/257,174
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: PCT/US01/11797
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: 60/196,603
;  PRIOR FILING DATE: 2000-04-13
;  PRIOR APPLICATION NUMBER: 60/199,417
;  PRIOR FILING DATE: 2000-04-24
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 3228
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-257-174-10

Alignment Scores:
Pred. No.:              0           Length:         3228
Score:                  5234.50     Matches:        1013
Percent Similarity:     95.68%      Conservative:   7
Best Local Similarity:  95.03%      Mismatches:     34
Query Match:            91.42%      Indels:         13
DB:                     19          Gaps:           3

US-09-833-222A-10 (1-1090) x US-10-257-174-10 (1-3228)

Qy         12 ArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyr 31
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 AGAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAATAC 117

Qy         32 SerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGlu 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATCGAG 177

Qy         52 GluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTGCGG 237

Qy         72 ArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAACCAC 297

Qy         92 GluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAsp 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGGGAC 357

Qy        112 GluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPhe 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 GAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCACTTC 417

Qy        132 SerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsn 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 AGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTACAAC 477

Qy        152 LysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheVal 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 AAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTCGTG 537

Qy        172 GluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhe 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 GAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGATTC 597

Qy        192 PheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAsp 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 TTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTTGAC 657

Qy        212 CysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeu 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 TGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATTTTG 717

Qy        232 ValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 GTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATCACC 777

Qy        252 ThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyr 271
              ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db        778 ACCATCTTGGACACCCTGGGGGAGAATGACTTCATTAATATCATAGCGTACAATGACTAC 837

Qy        272 ValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArg 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 GTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAATCGA 897

Qy        292 GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGln 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 GAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGACCAA 957

Qy        312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeu 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 GCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGCCTC 1017

Qy        332 CysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPhe 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 TGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTGTTT 1077

Qy        352 GluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGlu 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 GAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGAGAA 1137

Qy        372 ValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGln 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 GTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACGCAG 1197

Qy        392 IleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArg 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 ATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGCCGC 1257
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Qy       412 ProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLys 431
Db      1258 CCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGCAAG 1317

Qy       432 LeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPhe 451
Db      1318 CTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTCTTC 1377

Qy       452 SerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspVal 471
Db      1378 AGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGATGTG 1437

Qy       472 AlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAla 491
Db      1438 GCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATACGCC 1497

Qy       492 PheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArg 511
Db      1498 TTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTACAGA 1557

Qy       512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
Db      1558 GAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTGGAG 1617

Qy       532 TrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeu 551
Db      1618 TGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACTCTC 1677

Qy       552 SerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAsp 571
Db      1678 TCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAATGAC 1737

Qy       572 TyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGly 591
Db      1738 TACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGGGGC 1797

Qy       592 HisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeu 611
Db      1798 CACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTGCTT 1857

Qy       612 HisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAsp 631
Db      1858 CACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCAGAC 1917

Qy       632 HisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp 651
Db      1918 CACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCAGAC 1977

Qy       652 LeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaPro 671
Db      1978 CTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCCCCC 2037

Qy       672 MetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValVal 691
Db      2038 ATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTGGTG 2097

Qy       692 AspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySer 711
Db      2098 GACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCC 2157

Qy       712 GluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeu 731
Db      2158 GAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACCCTG 2217

Qy       732 AspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPhe 751
Db      2218 GACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTC 2277

Qy       752 AsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSer 771
Db      2278 AACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCAAGC 2337

Qy       772 ThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGln 791
Db      2338 ACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAA 2397

Qy       792 MetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrVal 811
Db      2398 ATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACTGTG 2457

Qy       812 AspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsn 831
Db      2458 GATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGACAAC 2517

Qy       832 AsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluVal 851
Db      2518 AACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTG 2577

Qy       852 AspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyr 871
Db      2578 GATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTAT 2637

Qy       872 AspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuVal 891
Db      2638 GACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTC 2697

Qy       892 SerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPhe 911
Db      2698 AGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTC 2757

Qy       912 LeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerVal 931
Db      2758 CTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCC--------- 2808

Qy       932 PheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyr 951
Db      2809 ------------CACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTAC 2856

Qy       952 ProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyPro 971
Db      2857 CCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCC 2916

Qy       972 CysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThr 991
Db      2917 TGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACA 2976

Qy       992 AspProThr---CysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010
Db      2977 GACCCCACCTTCTGCAGAATGGGCTCCGGTCCTGAGATATTGACCTTAACAGTGGCTTCT 3036

Qy      1011 LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgPro 1030
Db      3037 GCACATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACCA 3096

Qy      1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGly 1050
Db      3097 GACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGCGGCGCCTCGGAC 3156

Qy      1051 PheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
Db      3157 ACCTCAGCCTCGCCGCCCCTACTCCTGCT-GCCTGTGTGTGC-----------CTGGGG 3203

Qy      1071 MetProMetAsnThrPro 1076
Db      3204 GCTACTGCCCCAACTCCT 3221

RESULT 5
US-10-257-174-11
; Sequence 11, Application US/10257174
; Publication No. US20040034194A1
; GENERAL INFORMATION:
;  APPLICANT: Agarwal, Pankaj
;  APPLICANT:  Murdoch, Paul R.
;  APPLICANT:  Rizvi, Safia K.
;  APPLICANT:  Smith, Randall F.
```

```
;  APPLICANT:  Xiang, Zhaoying
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP50022
;  CURRENT APPLICATION NUMBER: US/10/257,174
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: PCT/US01/11797
;  PRIOR FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: 60/196,603
;  PRIOR FILING DATE: 2000-04-13
;  PRIOR APPLICATION NUMBER: 60/199,417
;  PRIOR FILING DATE: 2000-04-24
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 3345
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-257-174-11

Alignment Scores:
Pred. No.:              0           Length:         3345
Score:                  5230.50     Matches:        1012
Percent Similarity:     95.60%      Conservative:   8
Best Local Similarity:  94.85%      Mismatches:     35
Query Match:            91.35%      Indels:         13
DB:                     19          Gaps:           3

US-09-833-222A-10 (1-1090) x US-10-257-174-11 (1-3345)

Qy          11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
               :::   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         172 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 231

Qy          31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         232 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 291

Qy          51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         292 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 351

Qy          71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         352 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 411

Qy          91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         412 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 471

Qy         111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         472 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 531

Qy         131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         532 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 591

Qy         151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         592 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 651

Qy         171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         652 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 711

Qy         191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         712 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 771

Qy         211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         772 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 831

Qy         231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         832 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 891

Qy         251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
               ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db         892 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCATTAATATCATAGCGTACAATGAC 951

Qy         271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         952 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1011

Qy         291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1012 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1071

Qy         311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1072 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1131

Qy         331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1132 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1191

Qy         351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1192 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1251

Qy         371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1252 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1311

Qy         391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1312 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1371

Qy         411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1372 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1431

Qy         431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1432 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1491

Qy         451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1492 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1551

Qy         471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1552 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1611

Qy         491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1612 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1671

Qy         511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1672 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1731

Qy         531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1732 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1791

Qy         551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1792 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 1851

Qy         571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1852 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1911

Qy         591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
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Db       1912 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1971

Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630

Db       1972 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2031

Qy        631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650

Db       2032 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2091

Qy        651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670

Db       2092 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2151

Qy        671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690

Db       2152 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2211

Qy        691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710

Db       2212 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2271

Qy        711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730

Db       2272 TCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACC 2331

Qy        731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750

Db       2332 CTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTC 2391

Qy        751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770

Db       2392 TTCAACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCA 2451

Qy        771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyVal 790

Db       2452 AGCACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTC 2511

Qy        791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810

Db       2512 CAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACT 2571

Qy        811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830

Db       2572 GTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGAC 2631

Qy        831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850

Db       2632 AACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 2691

Qy        851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870

Db       2692 GTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATG 2751

Qy        871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890

Db       2752 TATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTG 2811

Qy        891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910

Db       2812 GTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTG 2871

Qy        911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930

Db       2872 TTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCC------ 2925

Qy        931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950

Db       2926 --------------CACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAG 2970

Qy        951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970

Db       2971 TACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGG 3030

Qy        971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990

Db       3031 CCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTG 3090

Qy        991 ThrAspProThr---CysAspCysSerIleProProValLeuGlnGluAlaThrGlu 1009

Db       3091 ACAGACCCCACCTTCTGCAGAATGGGCTCCGGTCCTGAGATATTGACCTTAACAGTGGCT 3150

Qy       1010 ValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArg 1029

Db       3151 TCTGCACATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGA 3210

Qy       1030 ProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049

Db       3211 CCAGACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGCGGCGCCTCG 3270

Qy       1050 GlyPheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIle 1069

Db       3271 GACACCTCAGCCTCGCCGCCCCTACTCCTGCT-GCCTGTGTGTGC-----------CTG 3317

Qy       1070 GlyMetProMetAsnThrPro 1076

Db       3318 GGGGCTACTGCCCCAACTCCT 3338
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RESULT 6
US-10-257-022-27
; Sequence 27, Application US/10257022
; Publication No. US20030211499A1
; GENERAL INFORMATION:
;  APPLICANT: REDDY, Roopa
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  BOROWSKY, Mark L.
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  SANJANWALA, Madhusudan M.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  NGUYEN, Danniel B.
;  APPLICANT:  POLICKY, Jennifer L.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  SEILHAMER, Jeffrey J.
;  APPLICANT:  WALIA, Narinder K.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  KEARNEY, Liam
;  APPLICANT:  WALSH, Roderick T.
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  LU, Yan
;  APPLICANT:  GREENE, Barrie D.
;  APPLICANT:  RAUMANN, Brigitte E.
;  APPLICANT:  Arvizu, Chandra S.
;  TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
;  FILE REFERENCE: PI-0067 USN
;  CURRENT APPLICATION NUMBER: US/10/257,022
;  CURRENT FILING DATE:  2002-10-04
;  PRIOR APPLICATION NUMBER: US01/11206
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/195,595
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/196,872
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: 60/199,020
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: 60/200,552
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 60/202,348
;  PRIOR FILING DATE: 2000-05-05
;  PRIOR APPLICATION NUMBER: 60/203,495
;  PRIOR FILING DATE: 2000-05-11
;  NUMBER OF SEQ ID NOS: 30
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;  SOFTWARE: PERL Program
; SEQ ID NO 27
;   LENGTH: 4125
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7473443CB1
US-10-257-022-27

Alignment Scores:
Pred. No.:                0              Length:          4125
Score:                    3808.00        Matches:         750
Percent Similarity:       80.90%         Conservative:    4
Best Local Similarity:    80.47%         Mismatches:      14
Query Match:              66.50%         Indels:          164
DB:                       18             Gaps:            2

US-09-833-222A-10 (1-1090) x US-10-257-022-27 (1-4125)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 1179

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 1239

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 1299

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1300 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 1359

Qy         91 HisGluPheAsnGluSerLeuVal---------------------------------- 98
              |||||||||||||||||||||||
Db       1360 CACGAATTCAATGAATCCCTGGTGGAACCTGGCGTGGGAGTTGGCGTGGGGATGTCCGTG 1419

Qy         98 ---------------------------------------------------------- 98

Db       1420 ACGCAGTCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGACGCAGTCCGGCGTGGGAGTT 1479

Qy         98 ---------------------------------------------------------- 98

Db       1480 GGCGTGGGGATGTCCATAACGCTGTCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGAGG 1539

Qy         98 ---------------------------------------------------------- 98

Db       1540 CAGTCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGACGCAGTCCGGCGTGGGAGTTGGC 1599

Qy         98 ---------------------------------------------------------- 98

Db       1600 GTGGGGATGTCCGTGACGCAGTCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGAGGCAG 1659

Qy         98 ---------------------------------------------------------- 98

Db       1660 TCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGACGCAGTCCTGGGGGGTGTTCAGTGCC 1719

Qy         98 ---------------------------------------------------------- 98

Db       1720 CAGCGCGCCGCCGCGGGTGCTTGTGTAGACTCTGATGGCCGCCCGGCCCCGGCCCTCTCG 1779

Qy         98 ---------------------------------------------------------- 98

Db       1780 TCCTCTCACCTGCGCCGTTTCTCTTCCTCTCTCTCCGCCTGTCCCGGTGCTCGGGCCGCC 1839

Qy         99 ----------------------------PheAspTyrTyrAsnSerValLeuIleAsnGlu 109
                                          ||||||||||||||||||||||||||||||||
Db       1840 TCCGTGGGCCTCACCCGTCCACCCCAGTTCGACTATTACAACTCGGTCCTGATCAACGAG 1899

Qy        110 ArgAspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAla 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1900 AGGGACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCT 1959

Qy        130 HisPheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnVal 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1960 CACTTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTG 2019

Qy        150 TyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaVal 169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2020 TACAACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTC 2079

Qy        170 PheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThr 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2080 TTCGTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACT 2139

Qy        190 GlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThr 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2140 GGATTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACT 2199

Qy        210 PheAspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleVal 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2200 TTTGACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTG 2259

Qy        230 IleLeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThr 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2260 ATTTTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACC 2319

Qy        250 IleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsn 269
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db       2320 ATCACCACCATCTTGGACACCCTGGGGGAGAATGACTTCATTAATATCATAGCGTACAAT 2379

Qy        270 AspTyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAsp 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2380 GACTACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGAC 2439

Qy        290 AsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValVal 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2440 AATCGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTG 2499

Qy        310 AspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGly 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2500 GACCAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGA 2559

Qy        330 SerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluPro 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2560 AGCCTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCG 2619

Qy        350 ValPheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGly 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2620 GTGTTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGG 2679

Qy        370 ArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyr 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2680 AGAGAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTAC 2739

Qy        390 ThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeu 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2740 ACGCAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTC 2799

Qy        410 SerArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAsp 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2800 AGCCGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGAC 2859

Qy        430 SerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetPro 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2860 AGCAAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCA 2919

Qy        450 ValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySer 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2920 GTCTTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCA 2979

Qy        470 AspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGly 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       2980 GATGTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGA 3039

Qy        490 TyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3040 TACGCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTG 3099

Qy        510 TyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGlu 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3100 TACAGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAA 3159

Qy        530 ValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGly 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3160 GTGGAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGT 3219

Qy        550 ThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThr 569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3220 ACTCTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACC 3279

Qy        570 AsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSer 589
              ||||||||||||||||||||||||||||||||||||||||||||||||    |||||||||||
Db       3280 AATGACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCC 3339

Qy        590 ArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAsp 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3340 CGGGGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGAC 3399

Qy        610 LeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAsp 629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3400 TTGCTTCACCCAGACTTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGAC 3459

Qy        630 ProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAsp 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3460 CCAGACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGAC 3519

Qy        650 ProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThr 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3520 CCAGACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACA 3579

Qy        670 AlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHis 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3580 GCCCCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACAC 3639

Qy        690 ValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheVal 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3640 GTGGTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTG 3699

Qy        710 GlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPhe 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3700 GGCTCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTC 3759

Qy        730 ThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3760 ACCCTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTC 3819

Qy        750 ValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThr 769
              ||||||||||||||||||||||||||||||||||          |||   |||
Db       3820 GTCTTCAACCTCCGCTGGGCAGAAGGACCA---------GGACGCCCTTCTGCCAAAGGC 3870

Qy        770 AlaSerThrAlaValAlaValThrValAspLysArg 781
                      :::     |||:::   ||||||
Db       3871 CTTCCACCACCACTTTGCCAAACCATCCTCAAGCGT 3906

RESULT 7
US-10-924-081-5
; Sequence 5, Application US/10924081
; Publication No. US20050095678A1
; GENERAL INFORMATION:
;  APPLICANT: PARKER, David
;  APPLICANT:  XU, Xianghong
;  APPLICANT:  KHAWAJA, Afsheen
;  APPLICANT:  SNUTCH, Terrance P.
;  TITLE OF INVENTION: NOVEL RAT CALCIUM CHANNEL SUBUNITS AND
;  TITLE OF INVENTION:  RELATED PROBES, CELL LINES AND METHODS
;  FILE REFERENCE: 381092001400
;  CURRENT APPLICATION NUMBER: US/10/924,081
;  CURRENT FILING DATE:  2004-08-23
;  PRIOR APPLICATION NUMBER: PCT/CA2004/001550
;  PRIOR FILING DATE: 2004-08-23
;  PRIOR APPLICATION NUMBER: US 60/497,096
;  PRIOR FILING DATE: 2003-08-22
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 3598
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-924-081-5

Alignment Scores:
Pred. No.:              0             Length:          3598
Score:                  3422.50       Matches:         626
Percent Similarity:     77.54%        Conservative:    192
Best Local Similarity:  59.34%        Mismatches:      220
Query Match:            59.77%        Indels:          18
DB:                     22            Gaps:            6

US-09-833-222A-10 (1-1090) x US-10-924-081-5 (1-3598)

Qy         13 ValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSer 32
              |||||||||||||||     |||||||||::::::   :::          |||||||||
Db        124 GTGAAGCTCTGGGCCTCCGCTTTTGGTGGGGAGATAAAATCCATTGCTGCCAAGTACTCG 183

Qy         33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
              ||||||   |||||||||||||||||||:::   |||      :::   |||||||||
Db        184 GGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATTGAAGAA 243

Qy         53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
              :::|||||||||:::|||||:::|||   :::::::::||||||   |||      :::
Db        244 ATCGACGGTCTCCAACTGGTGAAAAAGCTGGCCAAGAACATGGAAGAGATGTTTCACAAG 303

Qy         73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
              |||   |||||||||:::   ||||||||||||||||||||||   |||   ||||||
Db        304 AAGTCCGAGGCAGTGCGGCGTCTCGTGGAGGCTGCAGAGGAAGCACACCTGAAGCATGAA 363

Qy         93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
              |||:::      |||   ::::::|||:::|||:::|||||||||||||||||||:::
Db        364 TTTGACGCCGACTTGCAGTATGAATACTTCAATGCCGTGCTGATCAACGAGAGAGACAAA 423

Qy        113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
                 |||||||||:::|||||||||   |||||||:::|||      |||   ||||||:::
Db        424 GATGGGAACTTTTTGGAATTGGGAAAGGAGTTCATCTTGGCCCCCAATGACCATTTTAAT 483

Qy        133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
              ||||||||||||||   |||:::|||   ||||||:::|||||||||:::|||||||||
Db        484 AATTTGCCTGTGAACATCAGTCTGAGTGATGTCCAAGTGCCAACGAACATGTACAACAAA 543

Qy        153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
              ||||||   |||:::|||||||||||||   ||||||:::||||||   |||||||||:::
Db        544 GATCCTGCCATAGTCAATGGAGTGTATTGGTCTGAATCTCTAAACAAAGTTTTTGTAGAC 603

Qy        173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
              ||||||   |||||||||:::|||   |||||||||||||||||||   |||||||||
Db        604 AACTTCGATCGGGACCCGTCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTTTTC 663

Qy        193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
              |||   ||||||||||||||||   ||||||||||||||||||||   |||||||||
Db        664 AGACAGTACCCAGGGATTAAATGGGAACCAGACGAGAATGGAGTCATTGCCTTTGACTGC 723

Qy        213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
              |||||||||   ||||||||||||||||||||||||||||||:::||||||||||||||
Db        724 AGGAACAGGAAATGGTACATCCAGGCAGCAACTTCTCCAAAGGATGTGGTCATTTTGGTG 783

Qy        233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
              |||||||||||||||||||||||||||||||:::|||||||||||   |||:::::::::
Db        784 GACGTCAGCGGGAGCATGAAAGGACTCCGCCTGACCATCGCCAAGCAAACAGTCTCCTCG 843
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Qy 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db 844 ATACTGGACACCCTGGGCGATGATGACTTCTTCAACATCATCACGTATAACGAAGAGCTT 903
Qy 273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292
Db 904 CACTATGTGGAACCTTGTCTGAATGGAACACTGGTTCAAGCGGACAGGACCAACAAGGAG 963
Qy 293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
Db 964 CACTTCAGGGAGCATTTGGACAAACTTTTTGCCAAAGGGATTGGAATGCTCGATATTGCG 1023
Qy 313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
Db 1024 CTGAACGAGGCCTTCAATGTACTGAGCGATTTCAACCACACCGGACAAGGAAGCATTTGC 1083
Qy 333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
Db 1084 AGCCAGGCCATTATGCTCATAACCGATGGGGCAGTGGACACCTACGACACCATCTTTGCA 1143
Qy 353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db 1144 AAGTACAATTGGCCAGAGCGAAAGGTTCGAATCTTCACTTACCTCATTGGACGAGAGGCT 1203
Qy 373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
Db 1204 GCTTTTGCAGACAATCTCAAGTGGATGGCTTGTGCTAACAAAGGATTTTTCACCCAGATC 1263
Qy 393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
Db 1264 TCCACCTTGGCTGATGTGCAGGAAAATGTCATGGAATACCTCCATGTACTCAGTCGACCC 1323
Qy 413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
Db 1324 AAAGTCATCGACCAGGAACATGATGTGGTGTGGACCGAAGCGTACATCGACAGCACTCTC 1383
Qy 433 LeuSerSerGlnAla----------GlnSerLeuThrLeuLeuThrThrValAlaMet 448
Db 1384 CCTCAGGCTCAAAAGCTTGCTGATGATCAGGGCCTCGTCTTGATGACCACAGTGGCCATG 1443
Qy 449 ProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGly 468
Db 1444 CCTGTGTTTAGTAAGCAGAACGAAACTAGGTCAAAGGGCATTCTTCTGGGTGTGGTTGGC 1503
Qy 469 SerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHis 488
Db 1504 ACAGATGTCCCAGTAAAAGAGCTTCTGAAGACCATCCCCAAATACAAGTTAGGAATTCAT 1563
Qy 489 GlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgPro 508
Db 1564 GGTTATGCCTTTGCCATCACGAATAATGGATACATCTTGACACACCCGGAGCTCAGGCCC 1623
Qy 509 LeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSer 528
Db 1624 CTGTATGAAGAAGGGAAAAAG---CGAAGGAAGCCTAATTACAGTAGTGTGGATCTCTCG 1680
Qy 529 GluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThr 548
Db 1681 GAAGTCGAGTGGGAAGATCGGGATGATGTGTTACGAAATGCCATGGTGAATCGGAAGACT 1740
Qy 549 GlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeu 568
Db 1741 GGGAAATTCTCCATGGAAGTGAAGAAGACTGTGGACAAAGGGAAACGGGTTTTGGTGATG 1800
Qy 569 ThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeu 588
Db 1801 ACCAATGACTACTACTACACAGACATCAAGGGTGCTCCTTTCAGTTTAGGTGTGGCGCTC 1860
Qy 589 SerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHis 608
Db 1861 TCCAGGGGCCACGGGAAATACTTCTTCCGAGGGAATGTAACCATTGAAGAAGGGCTCCAT 1920
Qy 609 AspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIle 628
Db 1921 GACTTAGAACATCCTGACGTGTCCTTGGCAGATGAATGGTCCTACTGCAACACTGATCTG 1980
Qy 629 AspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLys 648
Db 1981 CACCCAGAGCACCGCCATCTCTCTCAACTGGAAGCGATTAAGCTCTACCTCAAAGGCAAG 2040
Qy 649 AspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValVal 668
Db 2041 GAGCCTCTGCTTCAATGTGACAAAGAATTGATTCAAGAAGTCCTTTTTGATGCTGTGGTA 2100
Qy 669 ThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGlu 688
Db 2101 AGCGCCCCTATCGAAGCCTATTGGACCAGCCTGGCCCTCAACAAATCTGAGAATTCTGAC 2160
Qy 689 HisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPhe 708
Db 2161 AAGGGTGTAGAGGTCGCCTTCCTCGGCACTCGCACAGGCCTCTCAAGAATCAACCTGTTT 2220
Qy 709 ValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerVal 728
Db 2221 GTGGGGGCTGAACAGCTCACCAATCAGGACTTTCTGAAGGCTAGAGACAAAGAGAACATT 2280
Qy 729 PheThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySer 748
Db 2281 TTCAACGCAGATCATTTCCCTCTCTGGTACAGAAGAGCTGCCGAGCAGATTCCAGGAAGT 2340
Qy 749 PheValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValVal 768
Db 2341 TTTGTCTACTCCATCCCCTTCAGCACAGGA------ACGGTCAACAAAAGCAATGTGGTG 2394
Qy 769 ThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAla 788
Db 2395 ACAGCAAGTACCTCCATCCAACTCCTGGATGAGCGAAAATCTCCTGTGGTGGCAGCTGTA 2454
Qy 789 GlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCys 808
Db 2455 GGCATTCAGATGAAACTTGAATTCTTCCAAAGGAAGTTCTGGATGGCCAGCAGACAGTGT 2514
Qy 809 SerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheVal 828
Db 2515 GCCTCCCTGGATGGTAAATGCTCCATAAGCTGCGACGATGAGACTGTGAACTGTTACCTC 2574
Qy 829 IleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeu 848
Db 2575 ATAGACAATAACGGGTTCATTCTGGTGTCTGAAGACTACACACAGACTGGAGATTTTTTT 2634
Qy 849 GlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnVal 868
Db 2635 GGTGAGGTCGAAGGAGCTGTCATGAACAAGTTGTTAACAATGGGCTCCTTTAAAAGAATA 2694
Qy 869 ThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGln 888
Db 2695 ACCTTGTATGACTACCAAGCCATGTGTAGAGCCAACAAGGAGAGTAGTGACAGTGCCCAC 2754
Qy 889 ProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeu 908
Db 2755 GGACTCCTGGACCCCTATAAGGCCTTCCTCTCTGCAGCCAAGTGGATAGTGACGGAACTT 2814
Qy 909 ValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAla 928
Db 2815 GTCTTGTTCCTGGTGGAGTTTAACCTTTGC---AGTTGGTGGCACTCTGACATGACAGCT 2871
Qy 929 LysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAsp 948
Db 2872 AAAGCC--------------------CAGAAACTGAAACAGACCCTGGAGCCTTGTGAT 2910
Qy 949 ThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGlu 968
Db 2911 ACTGAATACCCAGCCTTTGTTTCCGAACGCACCATCAAGGAGACCACAGGGAACATTGCT 2970
Qy 969 CysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeu 988

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Db       2971 TGTGAAGACTGCTCCAAGTCCTTTGTCATCCAGCAAATCCCAAGTAGCAATCTGTTCATG 3030

Qy        989 LeuValThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThr 1008
              :::|||   |||   :::|||   |||            |||:::
Db       3031 GTGGTGGTGGACAGTAGCTGTCTCTGTGAGTCTGTGGCTCCTATCACCATGGCACCCATT 3090

Qy       1009 GluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArg 1028
              |||:::::||||||   |||:::|||||:::|||:::::::::||||||:::||||||
Db       3091 GAAATCAGGTATAATGAATCCCTTAAGTGTGAACGGTTAAAGGCTCAGAAGATCAGACGA 3150

Qy       1029 ArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrp 1048
              ||||||:::|||||||||   ||||||||||||         |||   :::|||   |||
Db       3151 CGTCCGGAATCCTGCCACGGCTTCCATCCTGAGGA-------GAATGCGAGAGAGTGTGG 3203

Qy       1049 AlaGlyPheSerSerProAsnProLeuCysLeuGlyLeuCysPro 1063
                        ||||||   |||      |||        |||
Db       3204 GGGTGCATCAAGTCTCCAGGCCCAGGTGGCCTTGCTGCTGCTCCC 3248

RESULT 8
US-09-728-628-12
; Sequence 12, Application US/09728628
; Patent No. US20020009786A1
; GENERAL INFORMATION:
;  APPLICANT:  Tang, Y. Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Goodrich, Ryle
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION:  No. US20020009786A1el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE:  791CIP2C
;  CURRENT APPLICATION NUMBER: US/09/728,628
;  CURRENT FILING DATE:  2000-12-01
;  PRIOR APPLICATION NUMBER:  09/552,929
;  PRIOR FILING DATE:  2000-04-18
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  pt_FL_genes Version 2.0
; SEQ ID NO 12
;   LENGTH: 3528
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (213)..(3206)
US-09-728-628-12

Alignment Scores:
Pred. No.:              0           Length:         3528
Score:                  3421.50     Matches:        629
Percent Similarity:     77.83%      Conservative:   189
Best Local Similarity:  59.85%      Mismatches:     212
Query Match:            59.75%      Indels:         22
DB:                     9           Gaps:           7

US-09-833-222A-10 (1-1090) x US-09-728-628-12 (1-3528)

Qy         12 ArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyr 31
              ||||||||||||||||||      ||||||||::::::   :::         ||||||
Db         51 AGGGTGAAGCTCTGGGCCTCGGCTTTTGGTGGGGAGATAAAATCCATTGCTGCTAAGTAC 110

Qy         32 SerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGlu 51
              |||||||||   |||||||||||||||||||:::   |||      :::   ||||||
Db        111 TCCGGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAA 170

Qy         52 GluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 71
              |||:::|||||||||:::||||||:::|||   :::::::::|||||   |||
Db        171 GAAATCGATGGCCTCCAACTGGTAAAGAAGCTGGCAAAGAACATGGAAGAGATGTTTCAC 230

Qy         72 ArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHis 91
              :::|||   |||||||||:::   ||||||||||||||||||||||||   |||   |||
Db        231 AAGAAGTCTGAGGCCGTCAGGCGTCTGGTGGAGGCTGCAGAAGAAGCACACCTGAAACAT 290

Qy         92 GluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAsp 111
              ||||||:::   |||   :::::::|||:::|||:::|||||||||||||||||||||
Db        291 GAATTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAAGGGAC 350

Qy        112 GluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPhe 131
              :::   |||||||||:::|||||||||   ||||||:::|||      |||   ||||||
Db        351 AAAGACGGGAATTTTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCAAATGACCATTTT 410

Qy        132 SerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsn 151
              :::|||||||||||||||   |||:::|||   ||||||:::|||||||||:::||||||
Db        411 AATAATTTGCCTGTGAACATCAGTCTAAGTGACGTCCAAGTACCAACGAACATGTACAAC 470

Qy        152 LysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheVal 171
              |||||||||   |||:::||||||||||||||   ||||||:::||||||   |||||||||
Db        471 AAAGACCCTGCAATTGTCAATGGGGTTTATTGGTCTGAATCTCTAAACAAAGTTTTTGTA 530

Qy        172 GluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhe 191
              :::|||||||   ||||||||||:::|||   ||||||||||||||||||||   ||||||
Db        531 GATAACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTT 590

Qy        192 PheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAsp 211
              ||||||   ||||||||||||||||||   ||||||||||||||||||||   ||||||
Db        591 TTTAGGCAGTATCCGGGGATTAAATGGGAACCAGATGAGAATGGAGTCATTGCCTTCGAC 650

Qy        212 CysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeu 231
              ||||||||||||   ||||||||||||||||||||||||||||||:::|||||||||
Db        651 TGCAGGAACCGAAAATGGTACATCCAGGCAGCAACTTCTCCGAAAGACGTGGTCATTTTA 710

Qy        232 ValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251
              ||||||||||||||||||||||||||||||:::|||||||||||   |||::::::
Db        711 GTTGACGTCAGTGGCAGCATGAAAGGACTCCGTCTGACTATCGCGAAGCAAACAGTCTCA 770

Qy        252 ThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyr 271
              :::||||||||||||||||||:::::::||||||   ||||||||||||||||:::
Db        771 TCCATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTGCTTATAATGAGGAG 830

Qy        272 ValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArg 291
              :::|||||:::|||||||||      |||   ||||||||||||||||||   |||:::
Db        831 CTTCACTATGTGGAACCTTGCCTGAATGGAACTTTGGTGCAAGCCGACAGGACAAACAAA 890

Qy        292 GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGln 311
              |||||||||:::      ::::::::::|||      ||||||:::|||::::::|||
Db        891 GAGCACTTCAGGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTGGAATGTTGGATATA 950

Qy        312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeu 331
              ||||||   |||||||||   ||||||      |||                |||||||:::
Db        951 GCTCTGAATGAGGCCTTCAACATTCTGAGTGATTTCAACCACACGGGACAAGGAAGTATC 1010

Qy        332 CysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPhe 351
              |||:::|||||||||||||||||:::|||||||||||:::   |||:::   :::|||
Db       1011 TGCAGTCAGGCCATCATGCTCATAACTGATGGGGCGGTGGACACCTATGATACAATCTTT 1070

Qy        352 GluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGlu 371
                 ||||||||||||||||   |||||||||:::||||||||||||||||||||||
Db       1071 GCAAAATACAATTGGCCAGATCGAAAGGTTCGCATCTTCACATACCTCATTGGACGAGAG 1130

Qy        372 ValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGln 391
              :::|||||||||   :::||||||:::||||||   |||||||||:::::||||||
Db       1131 GCTGCGTTTGCAGACAATCTAAAGTGGATGGCCTGTGCCAACAAAGGATTTTTTACCCAA 1190

Qy        392 IleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArg 411
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db       1191 ATCTCCACCTTGGCTGATGTGCAGGAGAATGTCATGGAATACCTTCACGTGCTTAGCCGG 1250

Qy        412 ProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLys 431
              |||   ||||||:::   :::||||||::::::||||||||||||||:::||||||
Db       1251 CCCAAAGTCATCGACCAGGAGCATGATGTGGTGTGGACCGAAGCTTACATTGACAGCACT 1310

Qy        432 LeuLeuSerSerGlnAlaGlnSerLeuThr----------------LeuLeuThrThr 445
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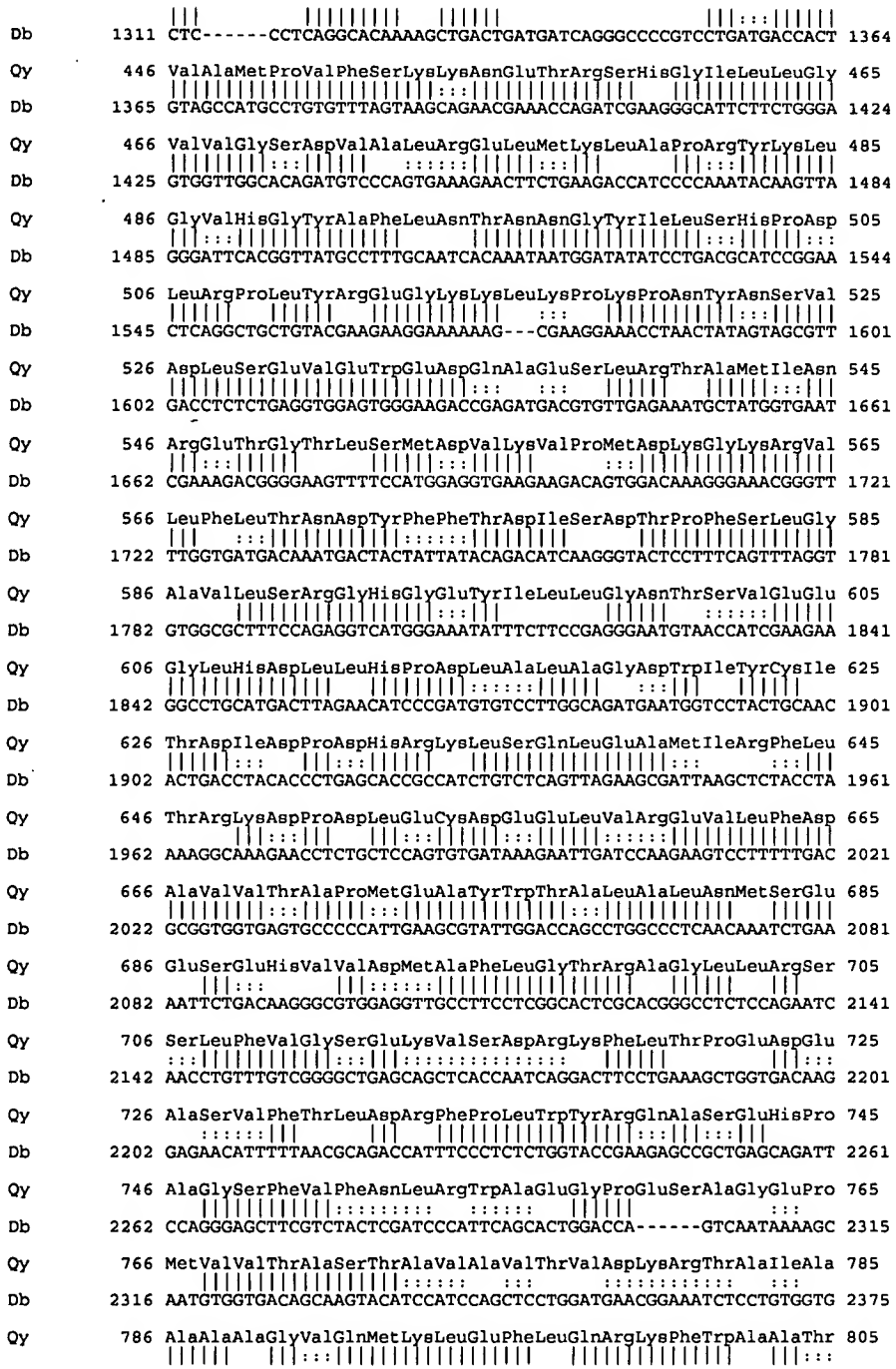

RESULT 9
US-10-972-024-117
; Sequence 117, Application US/10972024
; Publication No. US20050221342A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 791CIP4
; CURRENT APPLICATION NUMBER: US/10/972,024
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/US01/08655
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/668,317
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,783

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;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: 09/728,628
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 09/783,066
;  PRIOR FILING DATE: 2001-02-13
;  PRIOR APPLICATION NUMBER: 09/816,828
;  PRIOR FILING DATE: 2001-03-22
;  NUMBER OF SEQ ID NOS: 584
;  SOFTWARE: Custom
; SEQ ID NO 117
;   LENGTH: 3528
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (213)..(3203)
US-10-972-024-117

Alignment Scores:
Pred. No.:              0              Length:         3528
Score:                  3421.50        Matches:        629
Percent Similarity:     77.83%         Conservative:   189
Best Local Similarity:  59.85%         Mismatches:     212
Query Match:            59.75%         Indels:         22
DB:                     24             Gaps:           7

US-09-833-222A-10 (1-1090) x US-10-972-024-117 (1-3528)

Qy         12 ArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyr 31
              ||||||||||||||||||      ||||||||::::::  :::         ||||||
Db         51 AGGGTGAAGCTCTGGGCCTCGGCTTTTGGTGGGGAGATAAAATCCATTGCTGCTAAGTAC 110

Qy         32 SerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGlu 51
              |||||||||   ||||||||||||||||||||:::   |||       :::   ||||||
Db        111 TCCGGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAA 170

Qy         52 GluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 71
              |||:::||||||||:::||||||:::|||   :::::::::||||||   |||
Db        171 GAAATCGATGGCCTCCAACTGGTAAAGAAGCTGGCAAAGAACATGGAAGAGATGTTTCAC 230

Qy         72 ArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHis 91
              :::|||   |||||||||:::   ||||||||||||||||||||||||   |||   |||
Db        231 AAGAAGTCTGAGGCCGTCAGGCGTCTGGTGGAGGCTGCAGAAGAAGCACACCTGAAACAT 290

Qy         92 GluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAsp 111
              ||||||:::      |||   ::::::||:::|||:::|||||||||||||||||||||
Db        291 GAATTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAAGGGAC 350

Qy        112 GluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPhe 131
              :::   |||||||||:::|||||||||   |||||||:::|||       |||   ||||||
Db        351 AAAGACGGGAATTTTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCAAATGACCATTTT 410

Qy        132 SerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsn 151
              :::||||||||||||||||   |||:::|||   ||||||:::||||||||||:::||||||
Db        411 AATAATTTGCCTGTGAACATCAGTCTAAGTGACGTCCAAGTACCAACGAACATGTACAAC 470

Qy        152 LysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheVal 171
              |||||||||   |||:::||||||||||||   ||||||:::||||||   |||||||||
Db        471 AAAGACCCTGCAATTGTCAATGGGGTTTATTGGTCTGAATCTCTAAACAAAGTTTTTGTA 530

Qy        172 GluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhe 191
              :::||||||   ||||||||||:::|||   ||||||||||||||||||||   ||||||
Db        531 GATAACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTT 590

Qy        192 PheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAsp 211
              ||||||   ||||||||||||||||||   ||||||||||||||||||||   ||||||
Db        591 TTTAGGCAGTATCCGGGGATTAAATGGGAACCAGATGAGAATGGAGTCATTGCCTTCGAC 650

Qy        212 CysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeu 231
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||||||
Db        651 TGCAGGAACCGAAAATGGTACATCCAGGCAGCAACTTCTCCGAAAGACGTGGTCATTTTA 710

Qy        232 ValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251
              ||||||||||||||||||||||||||||||||||:::|||||||||||   |||||:::||||||
Db        711 GTTGACGTCAGTGGCAGCATGAAAGGACTCCGTCTGACTATCGCGAAGCAAACAGTCTCA 770

Qy        252 ThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyr 271
              :::||||||||||||||||||:::::||||||   |||||||||||||||||:::
Db        771 TCCATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTGCTTATAATGAGGAG 830

Qy        272 ValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArg 291
              :::||||||:::|||||||||      |||   ||||||||||||||||||   |||:::
Db        831 CTTCACTATGTGGAACCTTGCCTGAATGGAACTTTGGTGCAAGCCGACAGGACAAACAAA 890

Qy        292 GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGln 311
              |||||||||:::      ::::::::::|||      ||||||:::|||::::::|||
Db        891 GAGCACTTCAGGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTGGAATGTTGGATATA 950

Qy        312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeu 331
              ||||||   |||||||||   ||||||      |||           ||||||||:::
Db        951 GCTCTGAATGAGGCCTTCAACATTCTGAGTGATTTCAACCACACGGGACAAGGAAGTATC 1010

Qy        332 CysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPhe 351
              |||:::|||||||||||||||||:::|||||||||||:::   |||:::   :::|||
Db       1011 TGCAGTCAGGCCATCATGCTCATAACTGATGGGGCGGTGGACACCTATGATACAATCTTT 1070

Qy        352 GluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGlu 371
                 ||||||||||||||||   |||||||||:::||||||||||||||||||||||
Db       1071 GCAAAATACAATTGGCCAGATCGAAAGGTTCGCATCTTCACATACCTCATTGGACGAGAG 1130

Qy        372 ValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGln 391
              :::||||||||||   :::||||||:::||||||   ||||||||:::::||||||
Db       1131 GCTGCGTTTGCAGACAATCTAAAGTGGATGGCCTGTGCCAACAAAGGATTTTTTACCCAA 1190

Qy        392 IleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArg 411
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db       1191 ATCTCCACCTTGGCTGATGTGCAGGAGAATGTCATGGAATACCTTCACGTGCTTAGCCGG 1250

Qy        412 ProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLys 431
              |||   ||||||:::   :::||||||:::::||||||||||||||:::||||||
Db       1251 CCCAAAGTCATCGACCAGGAGCATGATGTGGTGTGGACCGAAGCTTACATTGACAGCACT 1310

Qy        432 LeuLeuSerSerGlnAlaGlnSerLeuThr----------------LeuLeuThrThr 445
              |||         |||||||||   ||||||              |||:::||||||
Db       1311 CTC------CCTCAGGCACAAAAGCTGACTGATGATCAGGGCCCCGTCCTGATGACCACT 1364

Qy        446 ValAlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGly 465
              ||||||||||||||||||||||:::||||||||||||||   ||||||||||||||
Db       1365 GTAGCCATGCCTGTGTTTAGTAAGCAGAACGAAACCAGATCGAAGGGCATTCTTCTGGGA 1424

Qy        466 ValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeu 485
              |||||||||:::|||||||   ::::::||||||:::|||      |||:::||||||||
Db       1425 GTGGTTGGCACAGATGTCCCAGTGAAAGAACTTCTGAAGACCATCCCCAAATACAAGTTA 1484

Qy        486 GlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAsp 505
              |||:::|||||||||||||||||||||||||||||||||||||:::|||||||:::
Db       1485 GGGATTCACGGTTATGCCTTTGCAATCACAAATAATGGATATATCCTGACGCATCCGGAA 1544

Qy        506 LeuArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerVal 525
              ||||||   ||||||   ||||||||||||   :::   ||||||||||||:::||||||
Db       1545 CTCAGGCTGCTGTACGAAGAAGGAAAAAAG---CGAAGGAAACCTAACTATAGTAGCGTT 1601

Qy        526 AspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsn 545
              ||||||||||||||||||||||||||:::   :::   ||||||   ||||||:::|||
Db       1602 GACCTCTCTGAGGTGGAGTGGGAAGACCGAGATGACGTGTTGAGAAATGCTATGGTGAAT 1661

Qy        546 ArgGluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgVal 565
              |||:::||||||      ||||||:::||||      :::||||||||||||||||||
Db       1662 CGAAAGACGGGGAAGTTTTCCATGGAGGTGAAGAAGACAGTGGACAAAGGGAAACGGGTT 1721

Qy        566 LeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGly 585
              |||   :::||||||||||||:::::||||||||||      ||||||||||||||||||
Db       1722 TTGGTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCCTTTCAGTTTAGGT 1781

Qy        586 AlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGlu 605
                    ||||||||||||||||||:::|||         ||||||   ::::::||||||
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Db       1782 GTGGCGCTTTCCAGAGGTCATGGGAAATATTTCTTCCGAGGGAATGTAACCATCGAAGAA 1841

Qy        606 GlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIle 625

Db       1842 GGCCTGCATGACTTAGAACATCCCGATGTGTCCTTGGCAGATGAATGGTCCTACTGCAAC 1901

Qy        626 ThrAspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeu 645

Db       1902 ACTGACCTACACCCTGAGCACCGCCATCTGTCTCAGTTAGAAGCGATTAAGCTCTACCTA 1961

Qy        646 ThrArgLysAspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAsp 665

Db       1962 AAAGGCAAAGAACCTCTGCTCCAGTGTGATAAAGAATTGATCCAAGAAGTCCTTTTTGAC 2021

Qy        666 AlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGlu 685

Db       2022 GCGGTGGTGAGTGCCCCCATTGAAGCGTATTGGACCAGCCTGGCCCTCAACAAATCTGAA 2081

Qy        686 GluSerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSer 705

Db       2082 AATTCTGACAAGGGCGTGGAGGTTGCCTTCCTCGGCACTCGCACGGGCCTCTCCAGAATC 2141

Qy        706 SerLeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGlu 725

Db       2142 AACCTGTTTGTCGGGGCTGAGCAGCTCACCAATCAGGACTTCCTGAAAGCTGGTGACAAG 2201

Qy        726 AlaSerValPheThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisPro 745

Db       2202 GAGAACATTTTTAACGCAGACCATTTCCCTCTCTGGTACCGAAGAGCCGCTGAGCAGATT 2261

Qy        746 AlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluPro 765

Db       2262 CCAGGGAGCTTCGTCTACTCGATCCCATTCAGCACTGGACCA------GTCAATAAAAGC 2315

Qy        766 MetValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAla 785

Db       2316 AATGTGGTGACAGCAAGTACATCCATCCAGCTCCTGGATGAACGGAAATCTCCTGTGGTG 2375

Qy        786 AlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThr 805

Db       2376 GCAGCTGTAGGCATTCAGATGAAACTTGAATTTTTCCAAAGGAAGTTCTGGACTGCCAGC 2435

Qy        806 ArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAsp 825

Db       2436 AGACAGTGTGCTTCCCTGGATGGCAAATGCTCCATCAGCTGTGATGATGAGACTGTGAAT 2495

Qy        826 CysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGly 845

Db       2496 TGTTACCTCATAGACAATAATGGATTTATTTTGGTGTCTGAAGACTACACACAGACTGGA 2555

Qy        846 ArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPhe 865

Db       2556 GACTTTTTTGGTGAGATCGAGGGAGCTGTGATGAACAAATTGCTAACAATGGGCTCCTTT 2615

Qy        866 SerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSer 885

Db       2616 AAAAGAATTACCCTTTATGACTACCAAGCCATGTGTAGAGCCAACAAGGAAAGCAGCGAT 2675

Qy        886 AlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeu 905

Db       2676 GGCGCCCATGGCCTCCTGGATCCTTATAATGCCTTCCTCTCTGCAGTAAAATGGATCATG 2735

Qy        906 GlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGly 925

Db       2736 ACAGAACTTGTCTTGTTCCTGGTGGAATTTAACCTCTGC---AGTTGGTGGCACTCCGAT 2792

Qy        926 AlaGluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGln 945

Db       2793 ATGACAGCTAAAGCC--------------------CAGAAATTGAAACAGACCCTGGAG 2831

Qy        946 ProCysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGly 965

Db       2832 CCTTGTGATACTGAATATCCAGCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGG 2891

Qy        966 IleValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsn 985

Db       2892 AATATTGCTTGTGAAGACTGCTCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAAC 2951

Qy        986 LeuLeuLeuLeuValThrAspProThrCysAspCysSerIleProProValLeuGln 1005

Db       2952 CTGTTCATGGTGGTGGTGGACAGCAGCTGCCTCTGTGAATCTGTGGCCCCCATCACCATG 3011

Qy       1006 GluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLys 1025

Db       3012 GCACCCATTGAAATCAGGTATAATGAATCCCTTAAGTGTGAACGTCTAAAGGCCCAGAAG 3071

Qy       1026 LeuArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAsp 1045

Db       3072 ATCAGAAGGCGCCCAGAATCTTGTCATGGCTTCCATCCTGAG------GAGAATGCAAGG 3125

Qy       1046 ArgGlyTrpAlaGlyPheSerSerProAsnPro 1056

Db       3126 GAGTG-TGGGGGTGCGCCGAGTCTCCAAGCCCA 3157
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RESULT 10
US-09-875-423-3
; Sequence 3, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-423-3

Alignment Scores:

Pred. No.:	0	Length:	3276
Score:	3416.50	Matches:	628
Percent Similarity:	77.81%	Conservative:	189
Best Local Similarity:	59.81%	Mismatches:	212
Query Match:	59.67%	Indels:	22
DB:	9	Gaps:	7

US-09-833-222A-10 (1-1090) x US-09-875-423-3 (1-3276)

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Qy          13 ValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSer 32

Db         124 GTGAAGCTCTGGGCCTCGGCTTTTGGTGGGGAGATAAAATCCATTGCTGCTAAGTACTCC 183

Qy          33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52

Db         184 GGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 243

Qy          53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72

Db         244 ATTGATGGCCTCCAACTGGTAAAGAAGCTGGCAAAGAACATGGAAGAGATGTTTCACAAG 303

Qy          73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92

Db         304 AAGTCTGAGGCCGTCAGGCGTCTGGTGGAGGCTGCAGAAGAAGCACACCTGAAACATGAA 363

Qy          93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112

Db         364 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAAGGGACAAA 423

Qy         113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
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Qy       847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db      2629 TTTTTTGGTGAGATCGAGGGAGCTGTGATGAACAAATTGCTAACAATGGGCTCCTTTAAA 2688

Qy       867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla 886
Db      2689 AGAATTACCCTTTATGACTACCAAGCCATGTGTAGAGCCAACAAGGAAAGCAGCGATGGC 2748

Qy       887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGln 906
Db      2749 GCCCATGGCCTCCTGGATCCTTATAATGCCTTCCTCTCTGCAGTAAAATGGATCATGACA 2808

Qy       907 GluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAla 926
Db      2809 GAACTTGTCTTGTTCCTGGTGGAATTTAACCTCTGC---AGTTGGTGGCACTCCGATATG 2865

Qy       927 GluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPro 946
Db      2866 ACAGCTAAAGCC----------CAGAAATTGAAACAGACCCTGGAGCCT 2904

Qy       947 CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle 966
Db      2905 TGTGATACTGAATATCCAGCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGGAAT 2964

Qy       967 ValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeu 986
Db      2965 ATTGCTTGTGAAGACTGCTCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAACCTG 3024

Qy       987 LeuLeuLeuValThrAspProThrCysAspCysSerIleProProValLeuGlnGlu 1006
Db      3025 TTCATGGTGGTGGTGGACAGCAGCTGCCTCTGTGAATCTGTGGCCCCCATCACCATGGCA 3084

Qy      1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
Db      3085 CCCATTGAAATCAGGTATAATGAATCCCTTAAGTGTGAACGTCTAAAGGCCCAGAAGATC 3144

Qy      1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046
Db      3145 AGAAGGCGCCCAGAATCTTGTCATGGCTTCCATCCTGAG------GAGAATGCAAGGGAG 3198

Qy      1047 GlyTrpAlaGlyPheSerSerProAsnPro 1056
Db      3199 TG-TGGGGGTGCGCCGAGTCTCCAAGCCCA 3227
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RESULT 11
US-10-162-012-16
; Sequence 16, Application US/10162012
; Publication No. US20030051660A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,012
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
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;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 09/928,530
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: PCT/US01/25475
;  PRIOR FILING DATE: 2001-08-15
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;  PRIOR FILING DATE: 2000-08-21
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;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: PCT/US01/26096
;  PRIOR FILING DATE: 2001-08-21
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;  PRIOR FILING DATE: 2001-03-28
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;  PRIOR FILING DATE: 2001-05-11
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;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
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US-10-162-012-16
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Qy       153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
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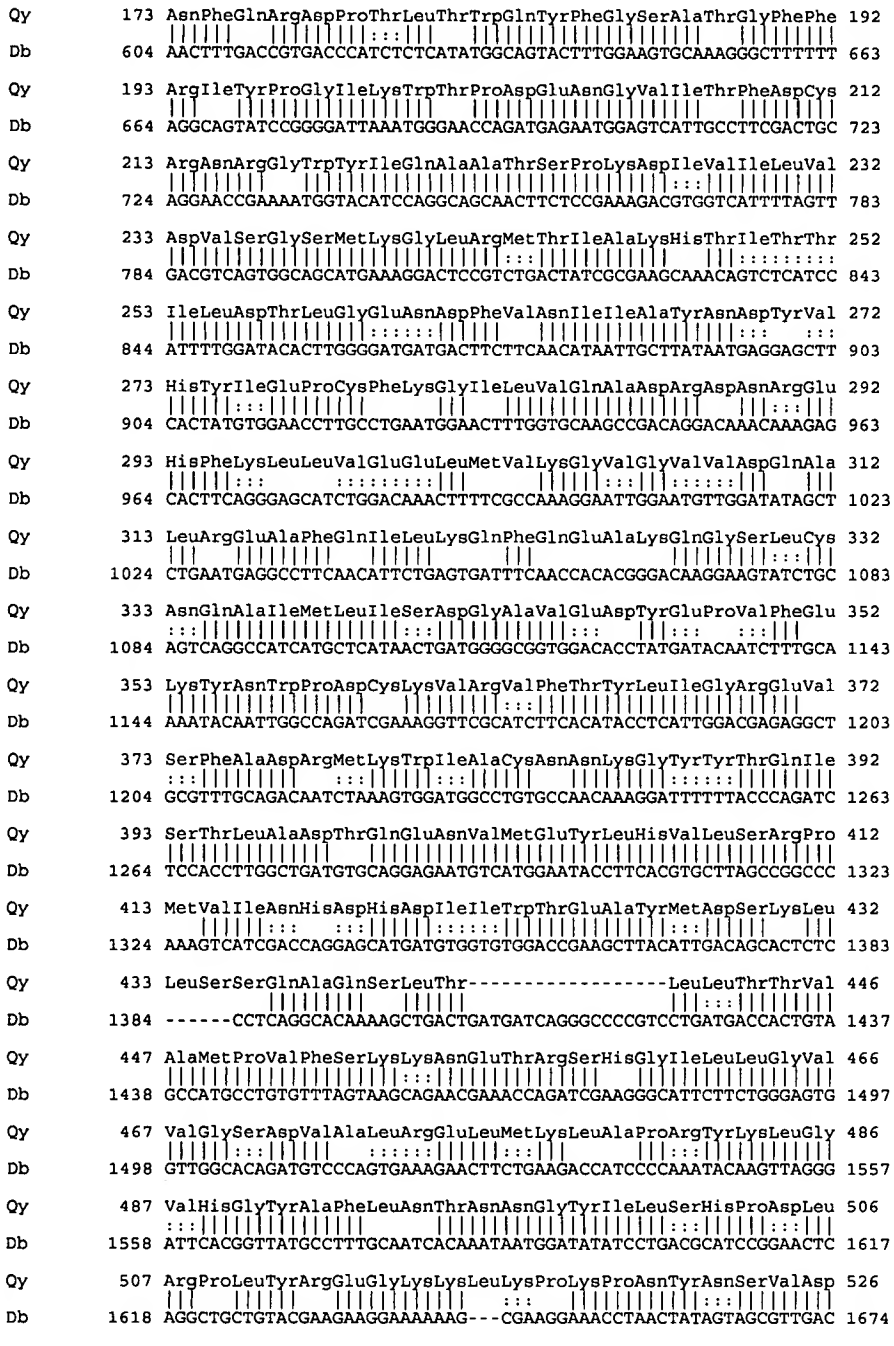
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; Publication No. US20030232336A1
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;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,102
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
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;  PRIOR FILING DATE: 2001-06-05
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;  PRIOR FILING DATE: 2000-08-22
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US-10-162-102-16

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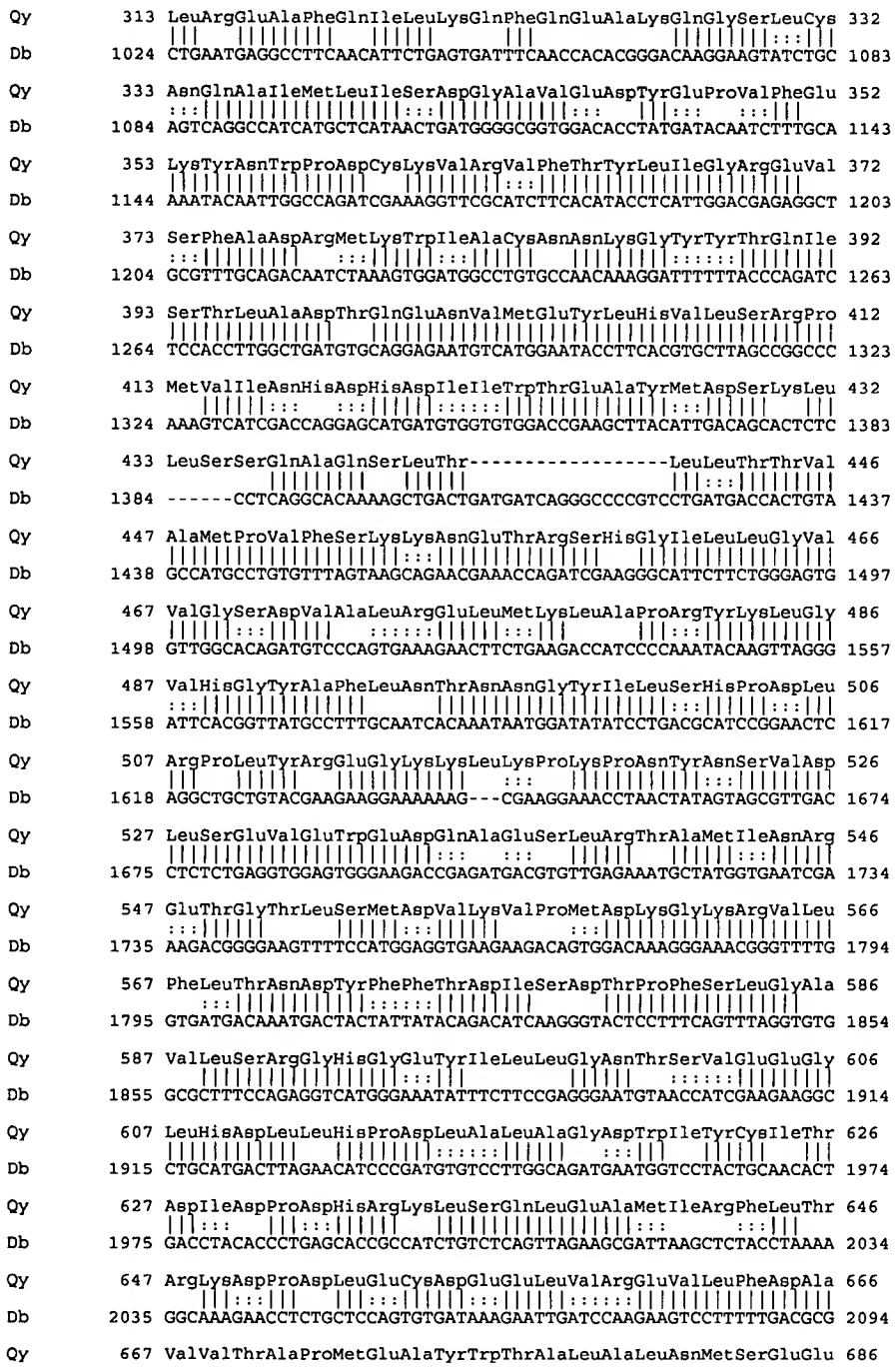
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Qy 767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
Db 2389 GTGGTGACAGCAAGTACATCCATCCAGCTCCTGGATGAACGGAAATCTCCTGTGGTGGCA 2448
Qy 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
Db 2449 GCTGTAGGCATTCAGATGAAACTTGAATTTTTCCAAAGGAAGTTCTGGACTGCCAGCAGA 2508
Qy 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
Db 2509 CAGTGTGCTTCCCTGGATGGCAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTGT 2568
Qy 827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
Db 2569 TACCTCATAGACAATAATGGATTTATTTTGGTGTCTGAAGACTACACACAGACTGGAGAC 2628
Qy 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db 2629 TTTTTTGGTGAGATCGAGGGAGCTGTGATGAACAAATTGCTAACAATGGGCTCCTTTAAA 2688
Qy 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla 886
Db 2689 AGAATTACCCTTTATGACTACCAAGCCATGTGTAGAGCCAACAAGGAAAGCAGCGATGGC 2748
Qy 887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGln 906
Db 2749 GCCCATGGCCTCCTGGATCCTTATAATGCCTTCCTCTCTGCAGTAAAATGGATCATGACA 2808
Qy 907 GluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAla 926
Db 2809 GAACTTGTCTTGTTCCTGGTGGAATTTAACCTCTGC---AGTTGGTGGCACTCCGATATG 2865
Qy 927 GluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPro 946
Db 2866 ACAGCTAAAGCC----------CAGAAATTGAAACAGACCCTGGAGCCT 2904
Qy 947 CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle 966
Db 2905 TGTGATACTGAATATCCAGCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGGAAT 2964
Qy 967 ValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeu 986
Db 2965 ATTGCTTGTGAAGACTGCTCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAACCTG 3024
Qy 987 LeuLeuLeuValThrAspProThrCysAspCysSerIleProProValLeuGlnGlu 1006
Db 3025 TTCATGGTGGTGGTGGACAGCAGCTGCCTCTGTGAATCTGTGGCCCCCATCACCATGGCA 3084
Qy 1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
Db 3085 CCCATTGAAATCAGGTATAATGAATCCCTTAAGTGTGAACGTCTAAAGGCCCAGAAGATC 3144
Qy 1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046

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Db       3145 AGAAGGCGCCCAGAATCTTGTCATGGCTTCCATCCTGAG------GAGAATGCAAGGGAG 3198

Qy       1047 GlyTrpAlaGlyPheSerSerProAsnPro 1056
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Db       3199 TG-TGGGGGTGCGCCGAGTCTCCAAGCCCA 3227

RESULT 13
US-09-875-423-1
; Sequence 1, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
;  TITLE OF INVENTION:  FAMILY MEMBER AND USES THEREOF
;  FILE REFERENCE: 10448-059001
;  CURRENT APPLICATION NUMBER: US/09/875,423
;  CURRENT FILING DATE:  2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3690
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)...(3301)
US-09-875-423-1

Alignment Scores:
Pred. No.:              0           Length:         3690
Score:                  3416.50     Matches:        628
Percent Similarity:     77.81%      Conservative:   189
Best Local Similarity:  59.81%      Mismatches:     212
Query Match:            59.67%      Indels:         22
DB:                     9           Gaps:           7

US-09-833-222A-10 (1-1090) x US-09-875-423-1 (1-3690)

Qy         13 ValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSer 32
              |||||||||||||||     |||||||||::::::   :::          |||||||||
Db        152 GTGAAGCTCTGGGCCTCGGCTTTTGGTGGGGAGATAAAATCCATTGCTGCTAAGTACTCC 211

Qy         33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
              ||||||   ||||||||||||||||||||:::   |||      :::   |||||||||
Db        212 GGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 271

Qy         53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
              :::|||||||||:::|||||||:::|||   :::::::::||||||  |||       :::
Db        272 ATTGATGGCCTCCAACTGGTAAAGAAGCTGGCAAAGAACATGGAAGAGATGTTTCACAAG 331

Qy         73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
              |||   |||||||||:::   |||||||||||||||||||||||||   |||   ||||||
Db        332 AAGTCTGAGGCCGTCAGGCGTCTGGTGGAGGCTGCAGAAGAAGCACACCTGAAACATGAA 391

Qy         93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
              |||:::     |||   ::::::|||:::|||:::|||||||||||||||||||:::
Db        392 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAAGGGACAAA 451

Qy        113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
                 |||||||||:::|||||||||   ||||||:::|||       |||   ||||||:::
Db        452 GACGGGAATTTTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCAAATGACCATTTTAAT 511

Qy        133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
              ||||||||||||||   |||:::|||   ||||||:::|||||||||:::|||||||||
Db        512 AATTTGCCTGTGAACATCAGTCTAAGTGACGTCCAAGTACCAACGAACATGTACAACAAA 571

Qy        153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
              ||||||   |||:::||||||||||||   ||||||:::||||||   |||||||||:::
Db        572 GACCCTGCAATTGTCAATGGGGTTTATTGGTCTGAATCTCTAAACAAAGTTTTTGTAGAT 631

Qy        173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
                 ||||||   ||||||||:::|||   ||||||||||||||||||||   |||||||||
Db        632 AACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTTTTT 691

Qy        193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
              |||   ||||||||||||||||||   ||||||||||||||||||||   |||||||||
Db        692 AGGCAGTATCCGGGGATTAAATGGGAACCAGATGAGAATGGAGTCATTGCCTTCGACTGC 751

Qy        213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
              |||||||||   ||||||||||||||||||||||||||||||:::||||||||||||
Db        752 AGGAACCGAAAATGGTACATCCAGGCAGCAACTTCTCCGAAAGACGTGGTCATTTTAGTT 811

Qy        233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
              ||||||||||||||||||||||||||||||:::||||||||||   |||:::::::::
Db        812 GACGTCAGTGGCAGCATGAAAGGACTCCGTCTGACTATCGCGAAGCAAACAGTCTCATCC 871

Qy        253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
              ||||||||||||||||||:::::||||||   |||||||||||||||||:::   :::
Db        872 ATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTGCTTATAATGAGGAGCTT 931

Qy        273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292
              ||||||:::|||||||||       |||   ||||||||||||||||||   |||:::|||
Db        932 CACTATGTGGAACCTTGCCTGAATGGAACTTTGGTGCAAGCCGACAGGACAAACAAAGAG 991

Qy        293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
              ||||||:::      :::::::::|||      ||||||:::|||::::::|||   |||
Db        992 CACTTCAGGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTGGAATGTTGGATATAGCT 1051

Qy        313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
              |||   |||||||||   ||||||    |||                |||||||||:::|||
Db       1052 CTGAATGAGGCCTTCAACATTCTGAGTGATTTCAACCACACGGGACAAGGAAGTATCTGC 1111

Qy        333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
              :::|||||||||||||||||:::|||||||||||:::   |||:::   :::|||
Db       1112 AGTCAGGCCATCATGCTCATAACTGATGGGGCGGTGGACACCTATGATACAATCTTTGCA 1171

Qy        353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
              ||||||||||||||||    |||||||||:::||||||||||||||||||||||||||
Db       1172 AAATACAATTGGCCAGATCGAAAGGTTCGCATCTTCACATACCTCATTGGACGAGAGGCT 1231

Qy        373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
              :::|||||||||   :::|||||:::|||||||   ||||||||:::::|||||||||
Db       1232 GCGTTTGCAGACAATCTAAAGTGGATGGCCTGTGCCAACAAAGGATTTTTTACCCAGATC 1291

Qy        393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db       1292 TCCACCTTGGCTGATGTGCAGGAGAATGTCATGGAATACCTTCACGTGCTTAGCCGGCCC 1351

Qy        413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
              ||||||:::   :::||||||::::::|||||||||||||||:::||||||   |||
Db       1352 AAAGTCATCGACCAGGAGCATGATGTGGTGTGGACCGAAGCTTACATTGACAGCACTCTC 1411

Qy        433 LeuSerSerGlnAlaGlnSerLeuThr----------------LeuLeuThrThrVal 446
                       |||||||||   ||||||                |||:::|||||||||
Db       1412 ------CCTCAGGCACAAAAGCTGACTGATGATCAGGGCCCCGTCCTGATGACCACTGTA 1465

Qy        447 AlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyVal 466
              ||||||||||||||||||:::|||||||||||||||   ||||||||||||||||||
Db       1466 GCCATGCCTGTGTTTAGTAAGCAGAACGAAACCAGATCGAAGGGCATTCTTCTGGGAGTG 1525

Qy        467 ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly 486
              ||||||:::||||||   ::::::||||||:::|||      |||:::||||||||||
Db       1526 GTTGGCACAGATGTCCCAGTGAAAGAACTTCTGAAGACCATCCCCAAATACAAGTTAGGG 1585

Qy        487 ValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeu 506
              :::|||||||||||||      ||||||||||||||||||||:::|||||||:::|||
Db       1586 ATTCACGGTTATGCCTTTGCAATCACAAATAATGGATATATCCTGACGCATCCGGAACTC 1645

Qy        507 ArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAsp 526
              |||   ||||||   ||||||||||||   :::   ||||||||||||:::|||||||||
Db       1646 AGGCTGCTGTACGAAGAAGGAAAAAAG---CGAAGGAAACCTAACTATAGTAGCGTTGAC 1702

Qy        527 LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg 546
              ||||||||||||||||||||||||:::   :::   ||||||   ||||||:::||||||
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Db       1703 CTCTCTGAGGTGGAGTGGGAAGACCGAGATGACGTGTTGAGAAATGCTATGGTGAATCGA 1762

Qy        547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu 566

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Qy        567 PheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla 586

Db       1823 GTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCCTTTCAGTTTAGGTGTG 1882

Qy        587 ValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGly 606

Db       1883 GCGCTTTCCAGAGGTCATGGGAAATATTTCTTCCGAGGGAATGTAACCATCGAAGAAGGC 1942

Qy        607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626

Db       1943 CTGCATGACTTAGAACATCCCGATGTGTCCTTGGCAGATGAATGGTCCTACTGCAACACT 2002

Qy        627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646

Db       2003 GACCTACACCCTGAGCACCGCCATCTGTCTCAGTTAGAAGCGATTAAGCTCTACCTAAAA 2062

Qy        647 ArgLysAspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAla 666

Db       2063 GGCAAAGAACCTCTGCTCCAGTGTGATAAAGAATTGATCCAAGAAGTCCTTTTTGACGCG 2122

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Db       2183 TCTGACAAGGGCGTGGAGGTTGCCTTCCTCGGCACTCGCACGGGCCTCTCCAGAATCAAC 2242

Qy        707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726

Db       2243 CTGTTTGTCGGGGCTGAGCAGCTCACCAATCAGGACTTCCTGAAAGCTGGCGACAAGGAG 2302

Qy        727 SerValPheThrLeuAspArgProLeuTrpTyrArgGlnAlaSerGluHisProAla 746

Db       2303 AACATTTTTAACGCAGACCATTTCCCTCTCTGGTACCGAAGAGCCGCTGAGCAGATTCCA 2362

Qy        747 GlySerPheValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMet 766

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Qy        767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786

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Qy        787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806

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Qy        807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826

Db       2537 CAGTGTGCTTCCCTGGATGGCAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTGT 2596

Qy        827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846

Db       2597 TACCTCATAGACAATAATGGATTTATTTTGGTGTCTGAAGACTACACACAGACTGGAGAC 2656

Qy        847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866

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Qy        867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla 886

Db       2717 AGAATTACCCTTTATGACTACCAAGCCATGTGTAGAGCCAACAAGGAAAGCAGCGATGGC 2776

Qy        887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGln 906

Db       2777 GCCCATGGCCTCCTGGATCCTTATAATGCCTTCCTCTCTGCAGTAAAATGGATCATGACA 2836

Qy        907 GluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAla 926

Db       2837 GAACTTGTCTTGTTCCTGGTGGAATTTAACCTCTGC---AGTTGGTGGCACTCCGATATG 2893

Qy        927 GluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPro 946

Db       2894 ACAGCTAAAGCC--------------------CAGAAATTGAAACAGACCCTGGAGCCT 2932

Qy        947 CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle 966

Db       2933 TGTGATACTGAATATCCAGCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGGAAT 2992

Qy        967 ValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeu 986

Db       2993 ATTGCTTGTGAAGACTGCTCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAACCTG 3052

Qy        987 LeuLeuLeuValThrAspProThrCysAspCysSerIleProProValLeuGlnGlu 1006

Db       3053 TTCATGGTGGTGGTGGACAGCAGCTGCCTCTGTGAATCTGTGGCCCCCATCACCATGGCA 3112

Qy       1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026

Db       3113 CCCATTGAAATCAGGTATAATGAATCCCTTAAGTGTGAACGTCTAAAGGCCCAGAAGATC 3172

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Db       3227 TG-TGGGGGTGCGCCGAGTCTCCAAGCCCA 3255
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RESULT 14
US-10-162-012-14
; Sequence 14, Application US/10162012
; Publication No. US20030051660A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Gu, Wei
;  TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
;  FILE REFERENCE: 10448-190001
;  CURRENT APPLICATION NUMBER: US/10/162,012
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: US 60/209,845
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: US 09/875,321
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: PCT/US01/18340
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/209,257
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,423
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18398
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/209,238
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: US 09/875,363
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: PCT/US01/18247
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/227,068
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 09/928,530
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: PCT/US01/25475
;  PRIOR FILING DATE: 2001-08-15
;  PRIOR APPLICATION NUMBER: US 60/226,770
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 09/934,421
;  PRIOR FILING DATE: 2001-08-21
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;  PRIOR APPLICATION NUMBER: PCT/US01/26096
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 60/279,281
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 10/109,029
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: PCT/US02/09728
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/290,288
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 3690
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)...(3301)
US-10-162-012-14

Alignment Scores:
Pred. No.:              0           Length:         3690
Score:                  3416.50     Matches:        628
Percent Similarity:     77.81%      Conservative:   189
Best Local Similarity:  59.81%      Mismatches:     212
Query Match:            59.67%      Indels:         22
DB:                     15          Gaps:           7

US-09-833-222A-10 (1-1090) x US-10-162-012-14 (1-3690)

Qy          13 ValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSer 32
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Db         152 GTGAAGCTCTGGGCCTCGGCTTTTGGTGGGGAGATAAAATCCATTGCTGCTAAGTACTCC 211

Qy          33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
               ||||||  |||||||||||||||||||:::  |||     :::  |||||||||
Db         212 GGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 271

Qy          53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
               :::|||||||||:::||||||:::|||  :::::::::||||||  |||     :::
Db         272 ATTGATGGCCTCCAACTGGTAAAGAAGCTGGCAAAGAACATGGAAGAGATGTTTCACAAG 331

Qy          73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
               |||  |||||||||:::  |||||||||||||||||||||||  |||  ||||||
Db         332 AAGTCTGAGGCCGTCAGGCGTCTGGTGGAGGCTGCAGAAGAAGCACACCTGAAACATGAA 391

Qy          93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
               |||:::     |||   ::::::|||:::|||:::|||||||||||||||||||:::
Db         392 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAAGGGACAAA 451

Qy         113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
               |||||||||:::|||||||   ||||||:::|||     |||  ||||||:::
Db         452 GACGGGAATTTTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCAAATGACCATTTTAAT 511

Qy         133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
               ||||||||||||||   |||:::|||   |||||||:::|||||||||:::|||||||||
Db         512 AATTTGCCTGTGAACATCAGTCTAAGTGACGTCCAAGTACCAACGAACATGTACAACAAA 571

Qy         153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
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Db         572 GACCCTGCAATTGTCAATGGGGTTTATTGGTCTGAATCTCTAAACAAAGTTTTTGTAGAT 631

Qy         173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
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Db         632 AACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTTTTT 691

Qy         193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
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Db         692 AGGCAGTATCCGGGGATTAAATGGGAACCAGATGAGAATGGAGTCATTGCCTTCGACTGC 751

Qy         213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
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Qy         233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
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Db         812 GACGTCAGTGGCAGCATGAAAGGACTCCGTCTGACTATCGCGAAGCAAACAGTCTCATCC 871

Qy         253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
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Qy         313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
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Qy         353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
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Qy         373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
               :::|||||||||  :::|||||:::|||||||  |||||||||:::::|||||||||
Db        1232 GCGTTTGCAGACAATCTAAAGTGGATGGCCTGTGCCAACAAAGGATTTTTTACCCAGATC 1291

Qy         393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
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Db        1292 TCCACCTTGGCTGATGTGCAGGAGAATGTCATGGAATACCTTCACGTGCTTAGCCGGCCC 1351

Qy         413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
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Qy         433 LeuSerSerGlnAlaGlnSerLeuThr----------------LeuLeuThrThrVal 446
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Qy         527 LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg 546
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Db       1883 GCGCTTTCCAGAGGTCATGGGAAATATTTCTTCCGAGGGAATGTAACCATCGAAGAAGGC 1942

Qy        607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626

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Qy        647 ArgLysAspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAla 666

Db       2063 GGCAAAGAACCTCTGCTCCAGTGTGATAAAGAATTGATCCAAGAAGTCCTTTTTGACGCG 2122

Qy        667 ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu 686

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Qy        947 CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle 966

Db       2933 TGTGATACTGAATATCCAGCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGGAAT 2992

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; Publication No. US20030232336A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,102
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)...(3301)
US-10-162-102-14

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Score:	3416.50	Matches:	628

Percent Similarity: 77.81% Conservative: 189
Best Local Similarity: 59.81% Mismatches: 212
Query Match: 59.67% Indels: 22
DB: 18 Gaps: 7

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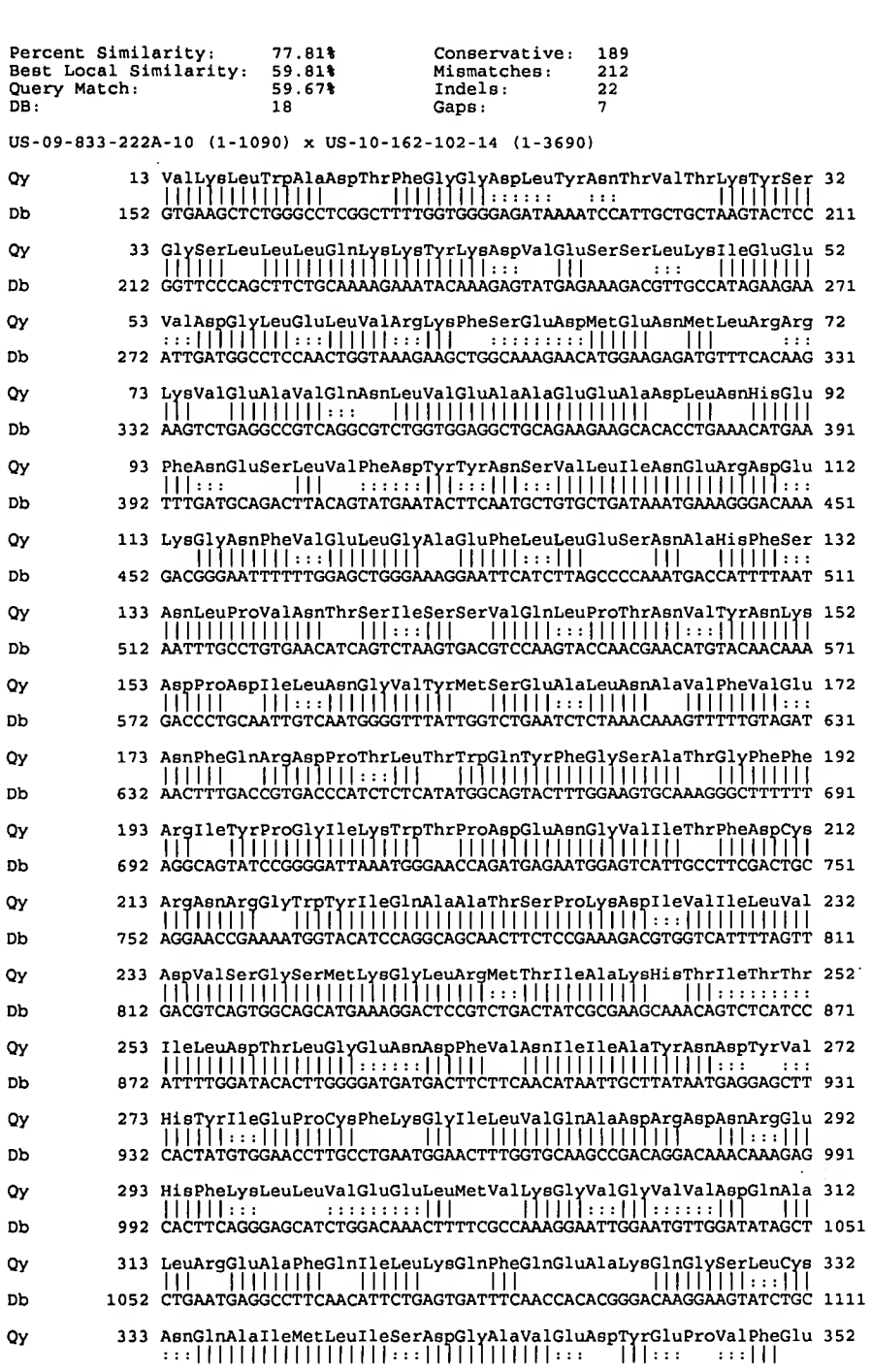

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Job time : 2153 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2005, 23:13:19 ; Search time 419 Seconds
(without alignments)
4256.663 Million cell updates/sec

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Perfect score: 5726
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Scoring table: BLOSUM62
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Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3416.5	59.7	3276	4	US-10-162-012-16	Sequence 16, Appl
2	3416.5	59.7	3690	4	US-10-162-012-14	Sequence 14, Appl
3	3410.5	59.6	3770	4	US-09-397-550-21	Sequence 21, Appl
4	3400.5	59.4	3213	4	US-09-397-550-9	Sequence 9, Appli
5	3326.5	58.1	3114	4	US-09-397-550-8	Sequence 8, Appli
6	3278.5	57.3	3057	4	US-09-397-550-7	Sequence 7, Appli
7	1792.5	31.3	1050	4	US-09-397-550-15	Sequence 15, Appl
8	1695	29.6	969	4	US-09-397-550-14	Sequence 14, Appl
9	1598	27.9	912	4	US-09-397-550-13	Sequence 13, Appl
10	1188.5	20.8	5279	3	US-09-470-443-5	Sequence 5, Appli
11	1187.5	20.7	5463	3	US-09-470-443-1	Sequence 1, Appli
12	1187.5	20.7	5482	3	US-09-470-443-3	Sequence 3, Appli
13	1187.5	20.7	5482	4	US-09-397-550-19	Sequence 19, Appl
14	1179.5	20.6	3327	4	US-09-397-550-3	Sequence 3, Appli
15	1158.5	20.2	3248	4	US-09-397-550-2	Sequence 2, Appli
16	1150.5	20.1	3186	4	US-09-397-550-1	Sequence 1, Appli
17	1089	19.0	3802	1	US-08-404-354B-2	Sequence 2, Appli
18	1089	19.0	3802	1	US-08-314-083B-2	Sequence 2, Appli
19	1089	19.0	3802	1	US-08-435-675B-2	Sequence 2, Appli
20	1089	19.0	3802	3	US-08-884-599-2	Sequence 2, Appli
21	1088	19.0	3802	1	US-08-336-257A-4	Sequence 4, Appli
22	1084	18.9	3579	1	US-08-455-543A-36	Sequence 36, Appl
23	1084	18.9	3579	2	US-08-193-078B-25	Sequence 25, Appl
24	1084	18.9	3579	2	US-08-223-305C-36	Sequence 36, Appl
25	1084	18.9	3579	3	US-08-949-386-32	Sequence 32, Appl
26	1084	18.9	3579	3	US-08-450-562-32	Sequence 32, Appl
27	1084	18.9	3579	3	US-08-984-709A-32	Sequence 32, Appl
28	1084	18.9	3579	3	US-08-450-272-32	Sequence 32, Appl
29	1084	18.9	3579	4	US-08-450-273-32	Sequence 32, Appl
30	1079.5	18.9	3636	1	US-08-455-543A-32	Sequence 32, Appl
31	1079.5	18.9	3636	2	US-08-193-078B-22	Sequence 22, Appl
32	1079.5	18.9	3636	2	US-08-223-305C-32	Sequence 32, Appl
33	1079.5	18.9	3636	3	US-08-949-386-29	Sequence 29, Appl
34	1079.5	18.9	3636	3	US-08-450-562-29	Sequence 29, Appl
35	1079.5	18.9	3636	3	US-08-984-709A-29	Sequence 29, Appl
36	1079.5	18.9	3636	3	US-08-450-272-29	Sequence 29, Appl
37	1079.5	18.9	3636	4	US-08-450-273-29	Sequence 29, Appl
38	1077.5	18.8	3566	1	US-07-745-206A-24	Sequence 24, Appl
39	1077.5	18.8	3566	2	US-08-311-363-24	Sequence 24, Appl
40	1077.5	18.8	3600	1	US-08-455-543A-11	Sequence 11, Appl
41	1077.5	18.8	3600	1	US-08-455-543A-33	Sequence 33, Appl
42	1077.5	18.8	3600	2	US-08-193-078B-11	Sequence 11, Appl
43	1077.5	18.8	3600	2	US-08-223-305C-11	Sequence 11, Appl
44	1077.5	18.8	3600	2	US-08-223-305C-33	Sequence 33, Appl
45	1077.5	18.8	3600	2	US-08-149-097D-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-162-012-16
; Sequence 16, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15

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;  PRIOR APPLICATION NUMBER: US 60/226,770
;  PRIOR FILING DATE: 2000-08-21
;  PRIOR APPLICATION NUMBER: US 09/934,421
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: PCT/US01/26096
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: US 60/279,281
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 10/109,029
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: PCT/US02/09728
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/290,288
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 3276
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-162-012-16

Alignment Scores:
Pred. No.:                0              Length:          3276
Score:                    3416.50        Matches:         628
Percent Similarity:       77.81%         Conservative:    189
Best Local Similarity:    59.81%         Mismatches:      212
Query Match:              59.67%         Indels:          22
DB:                       4              Gaps:            7

US-09-833-222A-10 (1-1090) x US-10-162-012-16 (1-3276)

Qy         13 ValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSer 32
              ||||||||||||||||      |||||||||::::::   :::          |||||||||
Db        124 GTGAAGCTCTGGGCCTCGGCTTTTGGTGGGGAGATAAAATCCATTGCTGCTAAGTACTCC 183

Qy         33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
              ||||||   ||||||||||||||||||||:::   |||      :::   |||||||||
Db        184 GGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 243

Qy         53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
              :::|||||||||:::|||||||:::|||   :::::::::||||||   |||       :::
Db        244 ATTGATGGCCTCCAACTGGTAAAGAAGCTGGCAAAGAACATGGAAGAGATGTTTCACAAG 303

Qy         73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
              |||   |||||||||:::   |||||||||||||||||||||||   |||   ||||||
Db        304 AAGTCTGAGGCCGTCAGGCGTCTGGTGGAGGCTGCAGAAGAAGCACACCTGAAACATGAA 363

Qy         93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
              |||:::      |||   ::::::|||:::|||:::|||||||||||||||||||:::
Db        364 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAAGGGACAAA 423

Qy        113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
                 |||||||||:::|||||||||   ||||||:::|||      |||   |||||||:::
Db        424 GACGGGAATTTTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCAAATGACCATTTTAAT 483

Qy        133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
              ||||||||||||||||   |||:::|||   |||||||:::|||||||||:::|||||||||
Db        484 AATTTGCCTGTGAACATCAGTCTAAGTGACGTCCAAGTACCAACGAACATGTACAACAAA 543

Qy        153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
              ||||||   |||:::|||||||||||   |||||||:::||||||   ||||||||||:::
Db        544 GACCCTGCAATTGTCAATGGGGTTTATTGGTCTGAATCTCTAAACAAAGTTTTTGTAGAT 603

Qy        173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
              ||||||   |||||||||:::|||   ||||||||||||||||||||   |||||||||
Db        604 AACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTTTTT 663

Qy        193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
              |||   ||||||||||||||||||   ||||||||||||||||||||||   |||||||||
Db        664 AGGCAGTATCCGGGGATTAAATGGGAACCAGATGAGAATGGAGTCATTGCCTTCGACTGC 723

Qy        213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
              ||||||||   ||||||||||||||||||||||||||||||||:::|||||||||||
Db        724 AGGAACCGAAAATGGTACATCCAGGCAGCAACTTCTCCGAAAGACGTGGTCATTTTAGTT 783

Qy        233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
              ||||||||||||||||||||||||||||||:::|||||||||||   |||:::::::::
Db        784 GACGTCAGTGGCAGCATGAAAGGACTCCGTCTGACTATCGCGAAGCAAACAGTCTCATCC 843

Qy        253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
              ||||||||||||||||||:::::|||||   ||||||||||||||||||:::   :::
Db        844 ATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTGCTTATAATGAGGAGCTT 903

Qy        273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292
              ||||||:::|||||||||      |||   ||||||||||||||||||   |||:::|||
Db        904 CACTATGTGGAACCTTGCCTGAATGGAACTTTGGTGCAAGCCGACAGGACAAACAAAGAG 963

Qy        293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
              ||||||:::      :::::::::|||      ||||||:::|||:::::::|||   |||
Db        964 CACTTCAGGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTGGAATGTTGGATATAGCT 1023

Qy        313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
              |||   |||||||||   ||||||      |||              ||||||||:::|||
Db       1024 CTGAATGAGGCCTTCAACATTCTGAGTGATTTCAACCACACGGGACAAGGAAGTATCTGC 1083

Qy        333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
              :::|||||||||||||||||:::||||||||||:::   |||:::   :::|||
Db       1084 AGTCAGGCCATCATGCTCATAACTGATGGGGCGGTGGACACCTATGATACAATCTTTGCA 1143

Qy        353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
              ||||||||||||||||   |||||||||:::|||||||||||||||||||||||||
Db       1144 AAATACAATTGGCCAGATCGAAAGGTTCGCATCTTCACATACCTCATTGGACGAGAGGCT 1203

Qy        373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
              :::|||||||||   :::|||||||:::||||||   |||||||||:::::|||||||||
Db       1204 GCGTTTGCAGACAATCTAAAGTGGATGGCCTGTGCCAACAAAGGATTTTTTACCCAGATC 1263

Qy        393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db       1264 TCCACCTTGGCTGATGTGCAGGAGAATGTCATGGAATACCTTCACGTGCTTAGCCGGCCC 1323

Qy        413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
                 ||||||:::   :::|||||||:::::|||||||||||||||:::|||||||   |||
Db       1324 AAAGTCATCGACCAGGAGCATGATGTGGTGTGGACCGAAGCTTACATTGACAGCACTCTC 1383

Qy        433 LeuSerSerGlnAlaGlnSerLeuThr----------------LeuLeuThrThrVal 446
                       |||||||||   ||||||   |||:::|||||||||
Db       1384 ------CCTCAGGCACAAAAGCTGACTGATGATCAGGGCCCCGTCCTGATGACCACTGTA 1437

Qy        447 AlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyVal 466
              |||||||||||||||||||:::|||||||||||||||   ||||||||||||||||||
Db       1438 GCCATGCCTGTGTTTAGTAAGCAGAACGAAACCAGATCGAAGGGCATTCTTCTGGGAGTG 1497

Qy        467 ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly 486
              ||||||:::||||||   ::::::||||||:::|||      |||:::|||||||||||
Db       1498 GTTGGCACAGATGTCCCAGTGAAAGAACTTCTGAAGACCATCCCCAAATACAAGTTAGGG 1557

Qy        487 ValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeu 506
              :::|||||||||||||||      ||||||||||||||||||||:::|||||:::|||
Db       1558 ATTCACGGTTATGCCTTTGCAATCACAAATAATGGATATATCCTGACGCATCCGGAACTC 1617

Qy        507 ArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAsp 526
              |||   ||||||   ||||||||||||   :::   ||||||||||||:::|||||||||
Db       1618 AGGCTGCTGTACGAAGAAGGAAAAAAG---CGAAGGAAACCTAACTATAGTAGCGTTGAC 1674

Qy        527 LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg 546
              ||||||||||||||||||||:::   :::   ||||||   ||||||:::||||||
Db       1675 CTCTCTGAGGTGGAGTGGGAAGACCGAGATGACGTGTTGAGAAATGCTATGGTGAATCGA 1734

Qy        547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu 566
              :::||||||      ||||||:::||||||      :::|||||||||||||||||||||
Db       1735 AAGACGGGGAAGTTTTCCATGGAGGTGAAGAAGACAGTGGACAAAGGGAAACGGGTTTTG 1794
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Qy       567 PheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla 586
Db      1795 GTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCCTTTCAGTTTAGGTGTG 1854

Qy       587 ValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGly 606
Db      1855 GCGCTTTCCAGAGGTCATGGGAAATATTTCTTCCGAGGGAATGTAACCATCGAAGAAGGC 1914

Qy       607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626
Db      1915 CTGCATGACTTAGAACATCCCGATGTGTCCTTGGCAGATGAATGGTCCTACTGCAACACT 1974

Qy       627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646
Db      1975 GACCTACACCCTGAGCACCGCCATCTGTCTCAGTTAGAAGCGATTAAGCTCTACCTAAAA 2034

Qy       647 ArgLysAspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAla 666
Db      2035 GGCAAAGAACCTCTGCTCCAGTGTGATAAAGAATTGATCCAAGAAGTCCTTTTTGACGCG 2094

Qy       667 ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu 686
Db      2095 GTGGTGAGTGCCCCCATTGAAGCGTATTGGACCAGCCTGGCCCTCAACAAATCTGAAAAT 2154

Qy       687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db      2155 TCTGACAAGGGCGTGGAGGTTGCCTTCCTCGGCACTCGCACGGGCCTCTCCAGAATCAAC 2214

Qy       707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726
Db      2215 CTGTTTGTCGGGGCTGAGCAGCTCACCAATCAGGACTTCCTGAAAGCTGGCGACAAGGAG 2274

Qy       727 SerValPheThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAla 746
Db      2275 AACATTTTTAACGCAGACCATTTCCCTCTCTGGTACCGAAGAGCCGCTGAGCAGATTCCA 2334

Qy       747 GlySerPheValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMet 766
Db      2335 GGGAGCTTCGTCTACTCGATCCCATTCAGCACTGGACCA------GTCAATAAAAGCAAT 2388

Qy       767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
Db      2389 GTGGTGACAGCAAGTACATCCATCCAGCTCCTGGATGAACGGAAATCTCCTGTGGTGGCA 2448

Qy       787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
Db      2449 GCTGTAGGCATTCAGATGAAACTTGAATTTTTCCAAAGGAAGTTCTGGACTGCCAGCAGA 2508

Qy       807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
Db      2509 CAGTGTGCTTCCCTGGATGGCAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTGT 2568

Qy       827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
Db      2569 TACCTCATAGACAATAATGGATTTATTTTGGTGTCTGAAGACTACACACAGACTGGAGAC 2628

Qy       847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db      2629 TTTTTTGGTGAGATCGAGGGAGCTGTGATGAACAAATTGCTAACAATGGGCTCCTTTAAA 2688

Qy       867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla 886
Db      2689 AGAATTACCCTTTATGACTACCAAGCCATGTGTAGAGCCAACAAGGAAAGCAGCGATGGC 2748

Qy       887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGln 906
Db      2749 GCCCATGGCCTCCTGGATCCTTATAATGCCTTCCTCTCTGCAGTAAAATGGATCATGACA 2808

Qy       907 GluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAla 926
Db      2809 GAACTTGTCTTGTTCCTGGTGGAATTTAACCTCTGC---AGTTGGTGGCACTCCGATATG 2865

Qy       927 GluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPro 946
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Db      2866 ACAGCTAAAGCC----------------------CAGAAATTGAAACAGACCCTGGAGCCT 2904

Qy       947 CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle 966
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Qy       967 ValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeu 986
Db      2965 ATTGCTTGTGAAGACTGCTCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAACCTG 3024

Qy       987 LeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGlu 1006
Db      3025 TTCATGGTGGTGGTGGACAGCAGCTGCCTCTGTGAATCTGTGGCCCCCATCACCATGGCA 3084

Qy      1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
Db      3085 CCCATTGAAATCAGGTATAATGAATCCCTTAAGTGTGAACGTCTAAAGGCCCAGAAGATC 3144

Qy      1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046
Db      3145 AGAAGGCGCCCAGAATCTTGTCATGGCTTCCATCCTGAG------GAGAATGCAAGGGAG 3198

Qy      1047 GlyTrpAlaGlyPheSerSerProAsnPro 1056
Db      3199 TG-TGGGGGTGCGCCGAGTCTCCAAGCCCA 3227
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RESULT 2
US-10-162-012-14
; Sequence 14, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28

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;  PRIOR APPLICATION NUMBER: PCT/US02/09728
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/290,288
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US (not assigned)
;  PRIOR FILING DATE: 2002-05-13
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 3690
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)...(3301)
US-10-162-012-14

Alignment Scores:
Pred. No.:              0           Length:         3690
Score:                  3416.50     Matches:        628
Percent Similarity:     77.81%      Conservative:   189
Best Local Similarity:  59.81%      Mismatches:     212
Query Match:            59.67%      Indels:         22
DB:                     4           Gaps:           7

US-09-833-222A-10 (1-1090) x US-10-162-012-14 (1-3690)

Qy         13 ValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSer 32
Db        152 GTGAAGCTCTGGGCCTCGGCTTTTGGTGGGGAGATAAAATCCATTGCTGCTAAGTACTCC 211

Qy         33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
Db        212 GGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 271

Qy         53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db        272 ATTGATGGCCTCCAACTGGTAAAGAAGCTGGCAAAGAACATGGAAGAGATGTTTCACAAG 331

Qy         73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
Db        332 AAGTCTGAGGCCGTCAGGCGTCTGGTGGAGGCTGCAGAAGAAGCACACCTGAAACATGAA 391

Qy         93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db        392 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAAGGGACAAA 451

Qy        113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
Db        452 GACGGGAATTTTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCAAATGACCATTTTAAT 511

Qy        133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
Db        512 AATTTGCCTGTGAACATCAGTCTAAGTGACGTCCAAGTACCAACGAACATGTACAACAAA 571

Qy        153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db        572 GACCCTGCAATTGTCAATGGGGTTTATTGGTCTGAATCTCTAAACAAAGTTTTTGTAGAT 631

Qy        173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db        632 AACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTTTTT 691

Qy        193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db        692 AGGCAGTATCCGGGGATTAAATGGGAACCAGATGAGAATGGAGTCATTGCCTTCGACTGC 751

Qy        213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
Db        752 AGGAACCGAAAATGGTACATCCAGGCAGCAACTTCTCCGAAAGACGTGGTCATTTTAGTT 811

Qy        233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252

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Qy        253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db        872 ATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTGCTTATAATGAGGAGCTT 931

Qy        273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292
Db        932 CACTATGTGGAACCTTGCCTGAATGGAACTTTGGTGCAAGCCGACAGGACAAACAAAGAG 991

Qy        293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
Db        992 CACTTCAGGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTGGAATGTTGGATATAGCT 1051

Qy        313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
Db       1052 CTGAATGAGGCCTTCAACATTCTGAGTGATTTCAACCACACGGGACAAGGAAGTATCTGC 1111

Qy        333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
Db       1112 AGTCAGGCCATCATGCTCATAACTGATGGGGCGGTGGACACCTATGATACAATCTTTGCA 1171

Qy        353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db       1172 AAATACAATTGGCCAGATCGAAAGGTTCGCATCTTCACATACCTCATTGGACGAGAGGCT 1231

Qy        373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
Db       1232 GCGTTTGCAGACAATCTAAAGTGGATGGCCTGTGCCAACAAAGGATTTTTTACCCAGATC 1291

Qy        393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
Db       1292 TCCACCTTGGCTGATGTGCAGGAGAATGTCATGGAATACCTTCACGTGCTTAGCCGGCCC 1351

Qy        413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
Db       1352 AAAGTCATCGACCAGGAGCATGATGTGGTGTGGACCGAAGCTTACATTGACAGCACTCTC 1411

Qy        433 LeuSerSerGlnAlaGlnSerLeuThr----------------LeuLeuThrThrVal 446
Db       1412 ------CCTCAGGCACAAAAGCTGACTGATGATCAGGGCCCCGTCCTGATGACCACTGTA 1465

Qy        447 AlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyVal 466
Db       1466 GCCATGCCTGTGTTTAGTAAGCAGAACGAAACCAGATCGAAGGGCATTCTTCTGGGAGTG 1525

Qy        467 ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly 486
Db       1526 GTTGGCACAGATGTCCCAGTGAAAGAACTTCTGAAGACCATCCCCAAATACAAGTTAGGG 1585

Qy        487 ValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeu 506
Db       1586 ATTCACGGTTATGCCTTTGCAATCACAAATAATGGATATATCCTGACGCATCCGGAACTC 1645

Qy        507 ArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAsp 526
Db       1646 AGGCTGCTGTACGAAGAAGGAAAAAAG---CGAAGGAAACCTAACTATAGTAGCGTTGAC 1702

Qy        527 LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg 546
Db       1703 CTCTCTGAGGTGGAGTGGGAAGACCGAGATGACGTGTTGAGAAATGCTATGGTGAATCGA 1762

Qy        547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu 566
Db       1763 AAGACGGGGAAGTTTTCCATGGAGGTGAAGAAGACAGTGGACAAAGGGAAACGGGTTTTG 1822

Qy        567 PheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla 586
Db       1823 GTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCCTTTCAGTTTAGGTGTG 1882

Qy        587 ValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGly 606
Db       1883 GCGCTTTCCAGAGGTCATGGGAAATATTTCTTCCGAGGGAATGTAACCATCGAAGAAGGC 1942
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Qy       607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626
Db      1943 CTGCATGACTTAGAACATCCCGATGTGTCCTTGGCAGATGAATGGTCCTACTGCAACACT 2002

Qy       627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646
Db      2003 GACCTACACCCTGAGCACCGCCATCTGTCTCAGTTAGAAGCGATTAAGCTCTACCTAAAA 2062

Qy       647 ArgLysAspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAla 666
Db      2063 GGCAAAGAACCTCTGCTCCAGTGTGATAAAGAATTGATCCAAGAAGTCCTTTTTGACGCG 2122

Qy       667 ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu 686
Db      2123 GTGGTGAGTGCCCCCATTGAAGCGTATTGGACCAGCCTGGCCCTCAACAAATCTGAAAAT 2182

Qy       687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db      2183 TCTGACAAGGGCGTGGAGGTTGCCTTCCTCGGCACTCGCACGGGCCTCTCCAGAATCAAC 2242

Qy       707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726
Db      2243 CTGTTTGTCGGGGCTGAGCAGCTCACCAATCAGGACTTCCTGAAAGCTGGCGACAAGGAG 2302

Qy       727 SerValPheThrLeuAspArgProLeuTrpTyrArgGlnAlaSerGluHisProAla 746
Db      2303 AACATTTTTAACGCAGACCATTTCCCTCTCTGGTACCGAAGAGCCGCTGAGCAGATTCCA 2362

Qy       747 GlySerPheValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMet 766
Db      2363 GGGAGCTTCGTCTACTCGATCCCATTCAGCACTGGACCA------GTCAATAAAAGCAAT 2416

Qy       767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
Db      2417 GTGGTGACAGCAAGTACATCCATCCAGCTCCTGGATGAACGGAAATCTCCTGTGGTGGCA 2476

Qy       787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
Db      2477 GCTGTAGGCATTCAGATGAAACTTGAATTTTTCCAAAGGAAGTTCTGGACTGCCAGCAGA 2536

Qy       807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
Db      2537 CAGTGTGCTTCCCTGGATGGCAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTGT 2596

Qy       827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
Db      2597 TACCTCATAGACAATAATGGATTTATTTTGGTGTCTGAAGACTACACACAGACTGGAGAC 2656

Qy       847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db      2657 TTTTTTGGTGAGATCGAGGGAGCTGTGATGAACAAATTGCTAACAATGGGCTCCTTTAAA 2716

Qy       867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla 886
Db      2717 AGAATTACCCTTTATGACTACCAAGCCATGTGTAGAGCCAACAAGGAAAGCAGCGATGGC 2776

Qy       887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGln 906
Db      2777 GCCCATGGCCTCCTGGATCCTTATAATGCCTTCCTCTCTGCAGTAAAATGGATCATGACA 2836

Qy       907 GluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAla 926
Db      2837 GAACTTGTCTTGTTCCTGGTGGAATTTAACCTCTGC---AGTTGGTGGCACTCCGATATG 2893

Qy       927 GluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPro 946
Db      2894 ACAGCTAAAGCC--------------------CAGAAATTGAAACAGACCCTGGAGCCT 2932

Qy       947 CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle 966
Db      2933 TGTGATACTGAATATCCAGCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGGAAT 2992

Qy       967 ValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeu 986
Db      2993 ATTGCTTGTGAAGACTGCTCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAACCTG 3052

Qy       987 LeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGlu 1006
Db      3053 TTCATGGTGGTGGTGGACAGCAGCTGCCTCTGTGAATCTGTGGCCCCCATCACCATGGCA 3112

Qy      1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
Db      3113 CCCATTGAAATCAGGTATAATGAATCCCTTAAGTGTGAACGTCTAAAGGCCCAGAAGATC 3172

Qy      1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046
Db      3173 AGAAGGCGCCCAGAATCTTGTCATGGCTTCCATCCTGAG-----GAGAATGCAAGGGAG 3226

Qy      1047 GlyTrpAlaGlyPheSerSerProAsnPro 1056
Db      3227 TG-TGGGGGTGCGCCGAGTCTCCAAGCCCA 3255

RESULT 3
US-09-397-550-21
; Sequence 21, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 3770
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-397-550-21

Alignment Scores:
Pred. No.:              0              Length:          3770
Score:                  3410.50        Matches:         624
Percent Similarity:     77.87%         Conservative:    189
Best Local Similarity:  59.77%         Mismatches:      216
Query Match:            59.56%         Indels:          16
DB:                     4              Gaps:            6

US-09-833-222A-10 (1-1090) x US-09-397-550-21 (1-3770)

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Qy         33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
Db        327 GGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 386

Qy         53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db        387 ATTGATGGCCTCCAACTGGTAAAGAAGCTGGCAAAGAACATGGAAGAGATGTTTCACAAG 446

Qy         73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
Db        447 AAGTCTGAGGCCGTCAGGCGTCTGGTGGAGGCTGCAGAAGAAGCACACCTGAAACATGAA 506

Qy         93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db        507 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAAGGGACAAA 566

Qy        113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
Db        567 GACGGGAATTTTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCAAATGACCATTTTAAT 626
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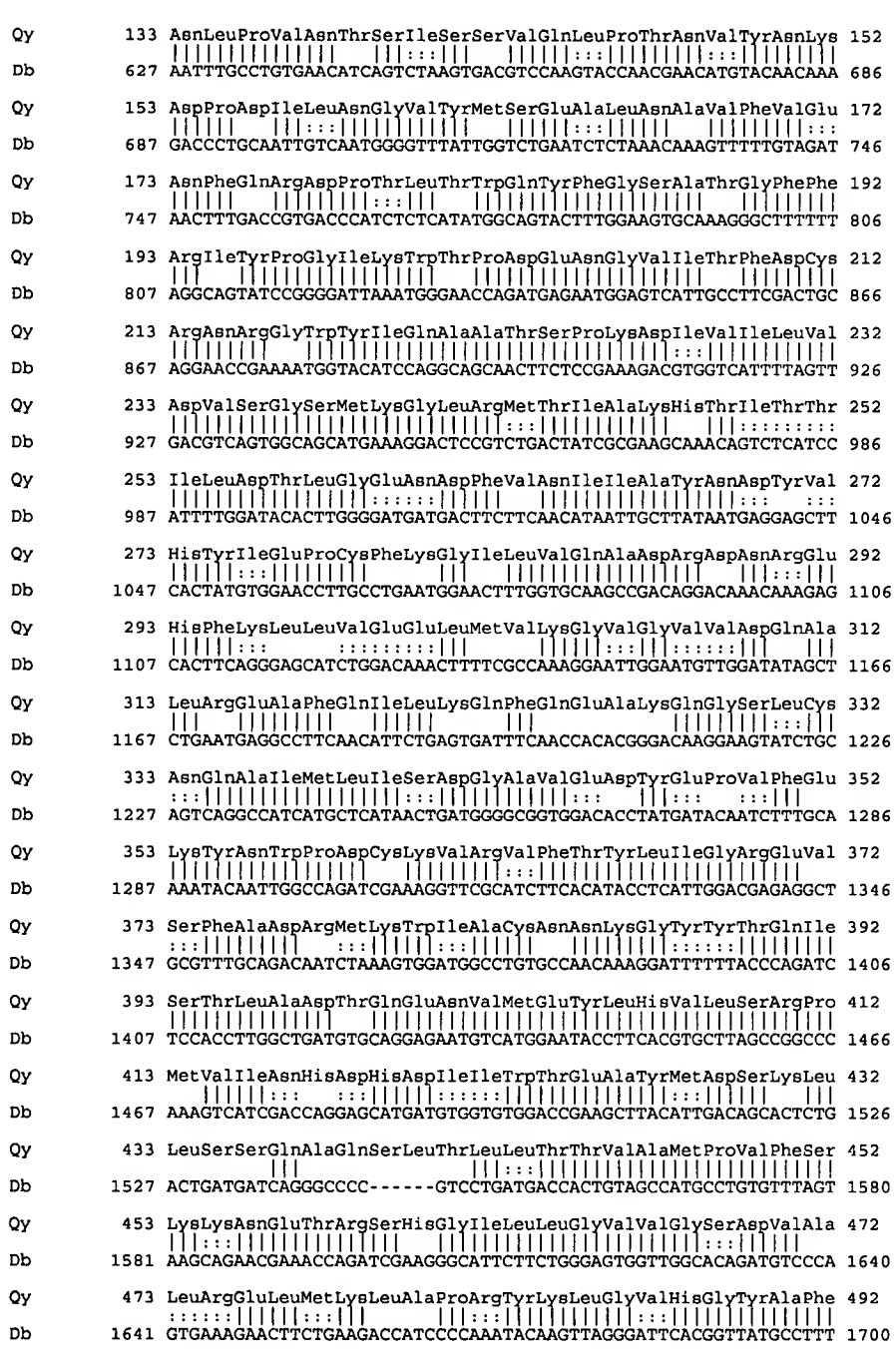
Qy 133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
Db 627 AATTTGCCTGTGAACATCAGTCTAAGTGACGTCCAAGTACCAACGAACATGTACAACAAA 686
Qy 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db 687 GACCCTGCAATTGTCAATGGGGTTTATTGGTCTGAATCTCTAAACAAAGTTTTTGTAGAT 746
Qy 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 747 AACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTTTTT 806
Qy 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db 807 AGGCAGTATCCGGGGATTAAATGGGAACCAGATGAGAATGGAGTCATTGCCTTCGACTGC 866
Qy 213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
Db 867 AGGAACCGAAAATGGTACATCCAGGCAGCAACTTCTCCGAAAGACGTGGTCATTTTAGTT 926
Qy 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db 927 GACGTCAGTGGCAGCATGAAAGGACTCCGTCTGACTATCGCGAAGCAAACAGTCTCATCC 986
Qy 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db 987 ATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTGCTTATAATGAGGAGCTT 1046
Qy 273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292
Db 1047 CACTATGTGGAACCTTGCCTGAATGGAACTTTGGTGCAAGCCGACAGGACAAACAAAGAG 1106
Qy 293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
Db 1107 CACTTCAGGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTGGAATGTTGGATATAGCT 1166
Qy 313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
Db 1167 CTGAATGAGGCCTTCAACATTCTGAGTGATTTCAACCACACGGGACAAGGAAGTATCTGC 1226
Qy 333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
Db 1227 AGTCAGGCCATCATGCTCATAACTGATGGGGCGGTGGACACCTATGATACAATCTTTGCA 1286
Qy 353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db 1287 AAATACAATTGGCCAGATCGAAAGGTTCGCATCTTCACATACCTCATTGGACGAGAGGCT 1346
Qy 373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
Db 1347 GCGTTTGCAGACAATCTAAAGTGGATGGCCTGTGCCAACAAAGGATTTTTTACCCAGATC 1406
Qy 393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
Db 1407 TCCACCTTGGCTGATGTGCAGGAGAATGTCATGGAATACCTTCACGTGCTTAGCCGGCCC 1466
Qy 413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
Db 1467 AAAGTCATCGACCAGGAGCATGATGTGGTGTGGACCGAAGCTTACATTGACAGCACTCTG 1526
Qy 433 LeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSer 452
Db 1527 ACTGATGATCAGGGCCCC------GTCCTGATGACCACTGTAGCCATGCCTGTGTTTAGT 1580
Qy 453 LysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAla 472
Db 1581 AAGCAGAACGAAACCAGATCGAAGGGCATTCTTCTGGGAGTGGTTGGCACAGATGTCCCA 1640
Qy 473 LeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPhe 492
Db 1641 GTGAAAGAACTTCTGAAGACCATCCCCAAATACAAGTTAGGGATTCACGGTTATGCCTTT 1700
Qy 493 LeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGlu 512
Db 1701 GCAATCACAAATAATGGRTATATCCTGACGCATCCGGAACTCAGGCTGCTGTACGAAGAA 1760
Qy 513 GlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGluTrp 532
Db 1761 GGAAAAAAG---CGAAGGAAACCTAACTATAGTAGCGTTGACCTCTCTGAGGTGGAGTGG 1817
Qy 533 GluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeuSer 552
Db 1818 GAAGACCGAGATGACGTGTTGAGAAATGCTATGGTGAATCGAAAGACGGGGAAGTTTTCC 1877
Qy 553 MetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAspTyr 572
Db 1878 ATGGAGGTGAAGAAGACAGTGGACAAAGGGAAACGGGTTTTGGTGATGACAAATGACTAC 1937
Qy 573 PhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHis 592
Db 1938 TATTATACAGACATCAAGGGTACTCCTTTCAGTTTAGGTGTGGCGCTTTCCAGAGGTCAT 1997
Qy 593 GlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHis 612
Db 1998 GGGAAATATTTCTTCCGAGGGAATGTAACCATCGAAGAAGGCCTGCATGACTTAGAACAT 2057
Qy 613 ProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHis 632
Db 2058 CCCGATGTGTCCTTGGCAGATGAATGGTCCTACTGCAACACTGACCTACACCCTGAGCAC 2117
Qy 633 ArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeu 652
Db 2118 CGCCATCTGTCTCAGTTAGAAGCGATTAAGCTCTACCTAAAAGGCAAAGAACCTCTGCTC 2177
Qy 653 GluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet 672
Db 2178 CAGTGTGATAAAGAATTGATCCAAGAAGTCCTTTTTGACGCGGTGGTGAGTGCCCCCATT 2237
Qy 673 GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp 692
Db 2238 GAAGCGTATTGGACCAGCCTGGCCCTCAACAAATCTGAAAATTCTGACAAGGGCGTGGAG 2297
Qy 693 MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu 712
Db 2298 GTTGCCTTCCTCGGCACTCGCACGGGCCTCTCCAGAATCAACCTGTTTGTCGGGGCTGAG 2357
Qy 713 LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp 732
Db 2358 CAGCTCACCAATCAGGACTTCCTGAAAGCTGGCGACAAGGAGAACATTTTTAACGCAGAC 2417
Qy 733 ArgProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsn 752
Db 2418 CATTTCCCTCTCTGGTACCGAAGAGCCGCTGAGCAGATTCCAGGGAGCTTCGTCTACTCG 2477
Qy 753 LeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThr 772
Db 2478 ATCCCATTCAGCACTGGACCA------GTCAATAAAAGCAATGTGGTGACAGCAAGTACA 2531
Qy 773 AlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMet 792
Db 2532 TCCATCCAGCTCCTGGATGAACGGAAATCTCCTGTGGTGGCAGCTGTAGGCATTCAGATG 2591
Qy 793 LysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAsp 812
Db 2592 AAACTTGAATTTTTCCAAAGGAAGTTCTGGACTGCCAGCAGACAGTGTGCTTCCCTGGAT 2651
Qy 813 GlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsn 832
Db 2652 GGCAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTGTTACCTCATAGACAATAAT 2711
Qy 833 GlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAsp 852
Db 2712 GGATTTATTTTGGTGTCTGAAGACTACACACAGACTGGAGACTTTTTTGGTGAGATCGAG 2771
Qy 853 GlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAsp 872

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Db       2772 GGAGCTGTGATGAACAAATTGCTAACAATGGGCTCCTTTAAAAGAATTACCCTTTATGAC 2831

Qy        873 TyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuValSer 892
Db       2832 TACCAAGCCATGTGTAGAGCCAACAAGGAAAGCAGCGATGGCGCCCATGGCCTCCTGGAT 2891

Qy        893 ProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeu 912
Db       2892 CCTTATAATGCCTTCCTCTCTGCAGTAAAATGGATCATGACAGAACTTGTCTTGTTCCTG 2951

Qy        913 LeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPhe 932
Db       2952 GTGGAATTTAACCTCTGC---AGTTGGTGGCACTCCGATATGACAGCTAAAGCC------ 3002

Qy        933 HisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrPro 952
Db       3003 --------------CAGAAATTGAAACAGACCCTGGAGCCTTGTGATACTGAATATCCA 3047

Qy        953 ValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys 972
Db       3048 GCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGGAATATTGCTTGTGAAGACTGC 3107

Qy        973 GlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAsp 992
Db       3108 TCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAACCTGTTCATGGTGGTGGTGGAC 3167

Qy        993 ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr 1012
Db       3168 AGCAGCTGCCTCTGTGAATCTGTGGCCCCCATCACCATGGCACCCATTGAAATCAGGTAT 3227

Qy       1013 AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgProAspSer 1032
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Qy       1033 CysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGlyPheSer 1052
Db       3288 TGTCATGGCTTCCATCCTGAG------GAGAATGCAAGGGAGTG-TGGGGGTGCGCCGAG 3340

Qy       1053 SerProAsnPro 1056
Db       3341 TCTCCAAGCCCA 3352
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RESULT 4
US-09-397-550-9
; Sequence 9, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-9

Alignment Scores:

Pred. No.:	0	Length:	3213
Score:	3400.50	Matches:	620
Percent Similarity:	78.12%	Conservative:	187
Best Local Similarity:	60.02%	Mismatches:	207
Query Match:	59.39%	Indels:	19
DB:	4	Gaps:	6

US-09-833-222A-10 (1-1090) x US-09-397-550-9 (1-3213)

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Qy          13 ValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSer 32
Db         124 GTGAAGCTCTGGGCCTCGGCTTTTGGTGGGGAGATAAAATCCATTGCTGCTAAGTACTCC 183

Qy          33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
Db         184 GGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 243

Qy          53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db         244 ATTGATGGCCTCCAACTGGTAAAGAAGCTGGCAAAGAACATGGAAGAGATGTTTCACAAG 303

Qy          73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
Db         304 AAGTCTGAGGCCGTCAGGCGTCTGGTGGAGGCTGCAGAAGAAGCACACCTGAAACATGAA 363

Qy          93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db         364 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAAGGGACAAA 423

Qy         113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
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Qy         133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
Db         484 AATTTGCCTGTGAACATCAGTCTAAGTGACGTCCAAGTACCAACGAACATGTACAACAAA 543

Qy         153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
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Qy         173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db         604 AACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTTTTT 663

Qy         193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db         664 AGGCAGTATCCGGGGATTAAATGGGAACCAGATGAGAATGGAGTCATTGCCTTCGACTGC 723

Qy         213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
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Qy         233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
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Qy         253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db         844 ATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTGCTTATAATGAGGAGCTT 903

Qy         273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292
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Qy         333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
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Qy         353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db        1144 AAATACAATTGGCCAGATCGAAAGGTTCGCATCTTCACATACCTCATTGGACGAGAGGCT 1203

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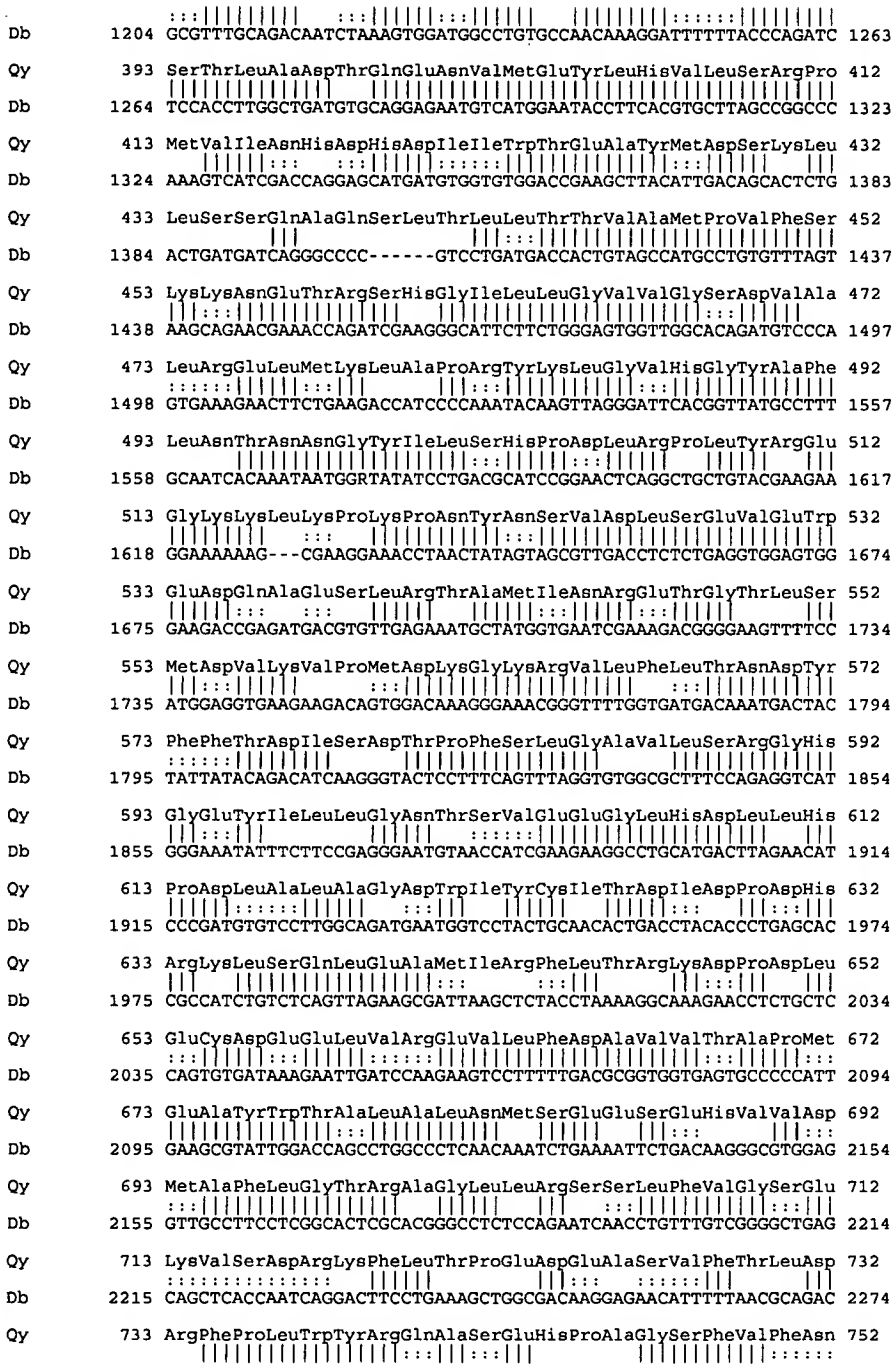

RESULT 5
US-09-397-550-8
; Sequence 8, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550

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;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 3114
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-397-550-8

Alignment Scores:
Pred. No.:                0                Length:          3114
Score:                    3326.50          Matches:         606
Percent Similarity:       78.32%           Conservative:    185
Best Local Similarity:    60.00%           Mismatches:      206
Query Match:              58.09%           Indels:          13
DB:                       4                Gaps:            5

US-09-833-222A-10 (1-1090) x US-09-397-550-8 (1-3114)

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Qy         33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
Db        184 GGTTCCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 243

Qy         53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db        244 ATTGATGGCCTCCAACTGGTAAAGAAGCTGGCAAAGAACATGGAAGAGATGTTTCACAAG 303

Qy         73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
Db        304 AAGTCTGAGGCCGTCAGGCGTCTGGTGGAGGCTGCAGAAGAAGCACACCTGAAACATGAA 363

Qy         93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db        364 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAAGGGACAAA 423

Qy        113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
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Qy        153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
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Db        724 AGGAACCGAAAATGGTACATCCAGGCAGCAACTTCTCCGAAAGACGTGGTCATTTTAGTT 783

Qy        233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db        784 GACGTCAGTGGCAGCATGAAAGGACTCCGTCTGACTATCGCGAAGCAAACAGTCTCATCC 843

Qy        253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db        844 ATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTGCTTATAATGAGGAGCTT 903

Qy        273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292

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Qy        293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
Db        964 CACTTCAGGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTGGAATGTTGGATATAGCT 1023

Qy        313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
Db       1024 CTGAATGAGGCCTTCAACATTCTGAGTGATTTCAACCACACGGGACAAGGAAGTATCTGC 1083

Qy        333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
Db       1084 AGTCAGGCCATCATGCTCATAACTGATGGGGCGGTGGACACCTATGATACAATCTTTGCA 1143

Qy        353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db       1144 AAATACAATTGGCCAGATCGAAAGGTTCGCATCTTCACATACCTCATTGGACGAGAGGCT 1203

Qy        373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
Db       1204 GCGTTTGCAGACAATCTAAAGTGGATGGCCTGTGCCAACAAAGGATTTTTTACCCAGATC 1263

Qy        393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
Db       1264 TCCACCTTGGCTGATGTGCAGGAGAATGTCATGGAATACCTTCACGTGCTTAGCCGGCCC 1323

Qy        413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
Db       1324 AAAGTCATCGACCAGGAGCATGATGTGGTGTGGACCGAAGCTTACATTGACAGCACTCTG 1383

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Qy        453 LysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAla 472
Db       1438 AAGCAGAACGAAACCAGATCGAAGGGCATTCTTCTGGGAGTGGTTGGCACAGATGTCCCA 1497

Qy        473 LeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPhe 492
Db       1498 GTGAAAGAACTTCTGAAGACCATCCCCAAATACAAGTTAGGGATTCACGGTTATGCCTTT 1557

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Qy        513 GlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGluTrp 532
Db       1618 GGAAAAAAG---CGAAGGAAACCTAACTATAGTAGCGTTGACCTCTCTGAGGTGGAGTGG 1674

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Qy        573 PhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHis 592
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Db      2095 GAAGCGTATTGGACCAGCCTGGCCCTCAACAAATCTGAAAATTCTGACAAGGGCGTGGAG 2154

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Qy       913 LeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPhe 932
Db      2809 GTGGAATTTAACCTCTGC---AGTTGGTGGCACTCCGATATGACAGCTAAAGCC------ 2859

Qy       933 HisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrPro 952
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Qy       953 ValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys 972
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Qy       973 GlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAsp 992
Db      2965 TCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAACCTGTTCATGGTGGTGGTGGAC 3024

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RESULT 6
US-09-397-550-7
; Sequence 7, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 3057
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-7

Alignment Scores:

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Score:	3278.50	Matches:	599
Percent Similarity:	78.51%	Conservative:	179
Best Local Similarity:	60.44%	Mismatches:	200
Query Match:	57.26%	Indels:	13
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US-09-833-222A-10 (1-1090) x US-09-397-550-7 (1-3057)

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Qy        53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
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Qy        73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
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Qy       113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
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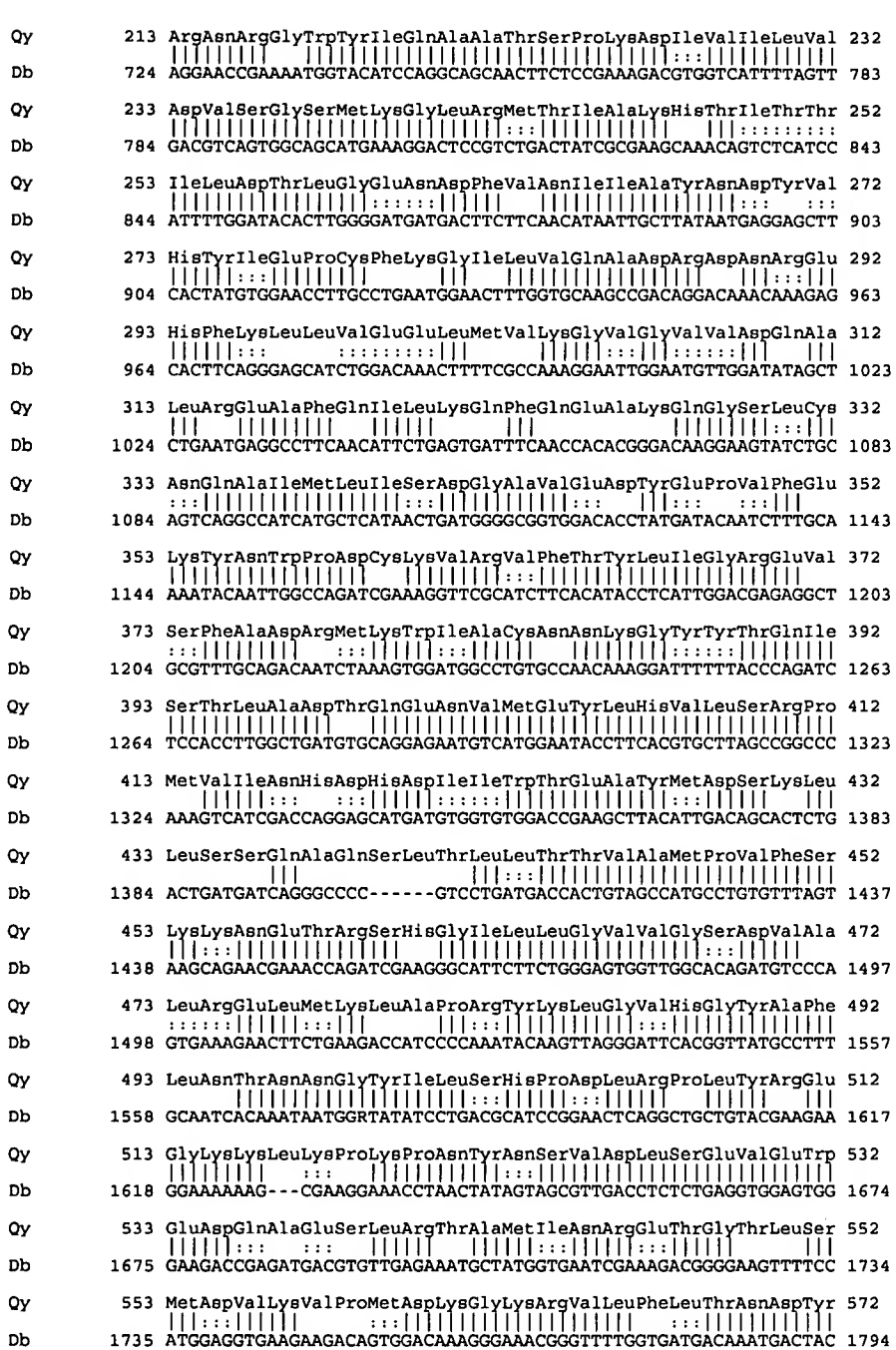
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Qy 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
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Qy 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
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Db 1795 TATTATACAGACATCAAGGGTACTCCTTTCAGTTTAGGTGTGGCGCTTTCCAGAGGTCAT 1854
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Qy 613 ProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHis 632
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Qy 633 ArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeu 652
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Qy 653 GluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet 672
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Qy 693 MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu 712
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Qy        953 ValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys 972
              ||||||   :::      |||:::|||      |||   :::   |||      |||
Db       2905 GCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGGAATATTGCTTGTGAAGACTGC 2964

Qy        973 GlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAsp 992
              |||   ||||||:::||||||||||||:::|||||||||   :::::::|||    |||
Db       2965 TCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAACCTGTTCATGGTGGTGGTGGAC 3024

Qy        993 ProThrCysAspCysSerIlePheProProVal 1003
                :::|||   |||            |||:::
Db       3025 AGCAGCTGCCTCTGTGAATCTGTGGCCCCCATC 3057

RESULT 7
US-09-397-550-15
; Sequence 15, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 1050
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-397-550-15

Alignment Scores:
Pred. No.:              4.77e-195      Length:          1050
Score:                  1792.50        Matches:         341
Percent Similarity:     98.00%         Conservative:    2
Best Local Similarity:  97.43%         Mismatches:      6
Query Match:            31.30%         Indels:          1
DB:                     4              Gaps:            1

US-09-833-222A-10 (1-1090) x US-09-397-550-15 (1-1050)

Qy        700 AlaGlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPhe 719
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGTCTCCGACAGGAAGTTC 60

Qy        720 LeuThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTrpTyrArg 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGACACCTGAGGACGAGGCCAGCGTGTTCACCCTGGACCGCTTCCCGCTGTGGTACCGC 120

Qy        740 GlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyPro 759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCTCCGCTGGGCAGAAGGACCA 180

Qy        760 GluSerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAsp 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAAGTGCGGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGTGGCGGTGACCGTGGAC 240

Qy        780 LysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArg 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGC 300

Qy        800 LysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys 819
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        301 AAATTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCCGTGCACACAGAGCTGC 360

Qy        820 GluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLys 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGACAGTGATCTGGACTGCTTCGTCATCGACAACAACGGGTTCATTCTGATCTCCAAG 420

Qy        840 ArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGCTGTCCTGACCCAGCTG 480

Qy        860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCAGGCCATGTGCAAACCC 540

Qy        880 SerSerHisHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACG 600

Qy        900 AlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGly 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGC 660

Qy        920 SerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLys 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCCTGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCACTCCCACAAACACAAG 720

Qy        940 LysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAla 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCC 780

Qy        960 IleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGln 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAG 840

Qy        980 GlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATC 900

Qy       1000 PheProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAsp 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTCCCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGCCTCTGTCAAATGTGAC 960

Qy       1020 ArgMetArgSerGlnLysLeuArgArgArgProAspSerCysHisAlaPheHisProGlu 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 CGGATGCGCTCCCAGAAGCTCCGCCGGCGACCAGACTCCTGCCACGCCTTCCATCCAGAG 1020

Qy       1040 ValArgValGluAlaAspArgGlyTrpAla 1049
                    :::   |||   |||   |||
Db       1021 GAGAATGCCCAG---GACTGCGGCGGCGCC 1047

RESULT 8
US-09-397-550-14
; Sequence 14, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 969
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-397-550-14

Alignment Scores:
Pred. No.:              6.27e-184      Length:          969
Score:                  1695.00        Matches:         321
Percent Similarity:     99.69%         Conservative:    1
Best Local Similarity:  99.38%         Mismatches:      1
Query Match:            29.60%         Indels:          0
DB:                     4              Gaps:            0

US-09-833-222A-10 (1-1090) x US-09-397-550-14 (1-969)
```

```
Qy        700 AlaGlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPhe 719
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGTCTCCGACAGGAAGTTC 60

Qy        720 LeuThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTrpTyrArg 739
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGACACCTGAGGACGAGGCCAGCGTGTTCACCCTGGACCGCTTCCCGCTGTGGTACCGC 120

Qy        740 GlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyPro 759
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCTCCGCTGGGCAGAAGGACCA 180

Qy        760 GluSerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAsp 779
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAAGTGCGGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGTGGCGGTGACCGTGGAC 240

Qy        780 LysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArg 799
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGC 300

Qy        800 LysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys 819
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAATTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCCGTGCACACAGAGCTGC 360

Qy        820 GluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLys 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGACAGTGATCTGGACTGCTTCGTCATCGACAACAACGGGTTCATTCTGATCTCCAAG 420

Qy        840 ArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 859
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGCTGTCCTGACCCAGCTG 480

Qy        860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCAGGCCATGTGCAAACCC 540

Qy        880 SerSerHisHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACG 600

Qy        900 AlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGly 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGC 660

Qy        920 SerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLys 939
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCCTGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCACTCCCACAAACACAAG 720

Qy        940 LysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAla 959
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCC 780

Qy        960 IleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGln 979
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAG 840

Qy        980 GlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATC 900

Qy       1000 PheProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAsp 1019
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTCCCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGCCTCTGTCAAATGTGAC 960

Qy       1020 ArgMetArg 1022
              |||||||||
Db        961 CGGATGCGC 969

RESULT 9
US-09-397-550-13
; Sequence 13, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 912
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-397-550-13

Alignment Scores:
Pred. No.:                7.47e-173      Length:          912
Score:                    1598.00        Matches:         302
Percent Similarity:       99.67%         Conservative:    1
Best Local Similarity:    99.34%         Mismatches:      1
Query Match:              27.91%         Indels:          0
DB:                       4              Gaps:            0

US-09-833-222A-10 (1-1090) x US-09-397-550-13 (1-912)

Qy        700 AlaGlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPhe 719
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGTCTCCGACAGGAAGTTC 60

Qy        720 LeuThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTrpTyrArg 739
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGACACCTGAGGACGAGGCCAGCGTGTTCACCCTGGACCGCTTCCCGCTGTGGTACCGC 120

Qy        740 GlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyPro 759
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCTCCGCTGGGCAGAAGGACCA 180

Qy        760 GluSerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAsp 779
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAAGTGCGGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGTGGCGGTGACCGTGGAC 240

Qy        780 LysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArg 799
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGC 300

Qy        800 LysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys 819
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAATTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCCGTGCACACAGAGCTGC 360

Qy        820 GluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLys 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGACAGTGATCTGGACTGCTTCGTCATCGACAACAACGGGTTCATTCTGATCTCCAAG 420

Qy        840 ArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 859
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGCTGTCCTGACCCAGCTG 480

Qy        860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCAGGCCATGTGCAAACCC 540

Qy        880 SerSerHisHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACG 600

Qy        900 AlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGly 919
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGC 660

Qy        920 SerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLys 939
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCCTGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCACTCCCACAAACACAAG 720
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Qy        940 LysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAla 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCC 780

Qy        960 IleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGln 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAG 840

Qy        980 GlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATC 900

Qy       1000 ProProVal 1003
              ||||||||||||
Db        901 TTCCCACCAGTG 912

RESULT 10
US-09-470-443-5
; Sequence 5, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
;  APPLICANT: Lerman, Michael I.
;  APPLICANT: Minna, John D.
;  APPLICANT: Latif, Farida
;  APPLICANT: Wei, Ming-Hui
;  APPLICANT: Sekido, Yoshitaka
;  APPLICANT: Gao, Boning
;  APPLICANT: Duh, Fuh-Mei
;  TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
;  FILE REFERENCE: NIH-05043
;  CURRENT APPLICATION NUMBER: US/09/470,443
;  CURRENT FILING DATE: 1999-12-22
;  EARLIER APPLICATION NUMBER: 60/114,359
;  EARLIER FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 5279
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (185)..(3415)
US-09-470-443-5

Alignment Scores:
Pred. No.:              1.63e-124      Length:         5279
Score:                  1188.50        Matches:        349
Percent Similarity:     47.61%         Conservative:   208
Best Local Similarity:  29.83%         Mismatches:     432
Query Match:            20.76%         Indels:         181
DB:                     3              Gaps:           44

US-09-833-222A-10 (1-1090) x US-09-470-443-5 (1-5279)

Qy         10 ArgAspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThr 29
              |||      ::::::  ||||||             ::::::         :::
Db        176 CGGGGGCTGATGCAGCACTGGGCCCGGCGTCTGGAGCAGGAGGTCGACGGCGTGATGCGG 235

Qy         30 LysTyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLys 49
                 :::   |||         |||::::::  |||||||      :::      :::
Db        236 ATTTTTGGAGGCGTCCAGCAGCTCCGTGAGATTTACAAGGACAACCGGAACCTGTTCGAG 295

Qy         50 IleGluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMet 69
              ::::::|||   :::      :::|||||  |||   :::   |||:::|||::::::
Db        296 GTACAGGAGAATGAGCCTCAGAAGTTGGTGGAGAAGGTGGCAGGGGACATTGAGAGCCTT 355

Qy         70 LeuArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeu 89
              |||   |||||||||:::|||::::::   |||   :::|||||||||
Db        356 CTGGACAGGAAGGTGCAGGCCCTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAA 415

Qy         90 AsnHisGluPheAsnGluSerLeuValPheAsp---------TyrTyrAsnSerValLeu 106
                 |||   :::   :::::::::      :::         ||||||::::::

Db        416 GCACACCGCTGGCAGGACAACATCAAGGAGGAAGACATCGTGTACTATGACGCCAAGGCT 475

Qy        107 IleAsnGluArgAspGlu---LysGlyAsnPheValGluLeuGlyAla------------ 121
                    |||   |||:::   :::         ||||||   |||:::
Db        476 GACGCTGAGCTGGACGACCCTGAGAGTGAGGATGTGGAAAGGGGGTCTAAGGCCAGCACC 535

Qy        122 ---------GluPheLeuLeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThr 138
                      :::|||:::   :::  |||     |||   |||     ||||||
Db        536 CTAAGGCTGGACTTCATCGAGGACCCAAAC------TTCAAGAAC---AAGGTCAACTAT 586

Qy        139 SerIleSerSerValGlnLeuProThrAsnValTyrAsnLysAspProAspIleLeuAsn 158
              |||   ::::::||||||:::||||||::::::|||                |||||||||
Db        587 TCATACGCGGCTGTACAGATCCCTACGGACATCTACAAAGGCTCCACTGTCATCCTCAAT 646

Qy        159 GlyValTyrMetSerGluAlaLeuAsnAlaValPheValGluAsnPheGlnArgAspPro 178
                 :::      :::|||||||||      ||||||:::|||||   ::::::||||||
Db        647 GAGCTCAACTGGACAGAGGCCCTGGAGAATGTGTTCATGGAAAACCGCAGACAAGACCCC 706

Qy        179 ThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArgIleTyrProGlyIle 198
              ||||||  ||||||  ||||||||||||||||||      |||  ||||||
Db        707 ACACTGCTGTGGCAGGTCTTCGGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACC 766

Qy        199 LysTrpThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyr 218
                 |||         :::      :::      :::|||   |||   |||   ||||||
Db        767 CCGTGGCGAGCCCCCAAGAAG---ATCGACCTGTACGATGTCCGAAGGAGACCCTGGTAT 823

Qy        219 IleGlnAlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMet 238
              ||||||   |||:::||||||||||:::||||||:::|||||||||||||||||||:::
Db        824 ATCCAGGGGGCCTCGTCACCCAAAGACATGGTCATCATCGTGGATGTGAGTGGCAGTGTG 883

Qy        239 LysGlyLeuArgMetThrIleAlaLysHisThrIleThrThrIleLeuAspThrLeuGly 258
                 ||||||  :::   :::   |||   ::::::        :::||||||||||||
Db        884 AGCGGCCTGACCCTGAAGCTGATGAAGACATCTGTCTGCGAGATGCTGGACACGCTGTCT 943

Qy        259 GluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrValHisTyrIleGluProCys 278
              ::::::|||:::||||||:::   ::::::|||:::            :::      |||
Db        944 GATGATGACTATGTGAATGTGGCCTCGTTCAACGAGAAGGCACAGCCTGTGTCA---TGC 1000

Qy        279 PheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuVal 298
              |||         ||||||||||:::      |||::::::   ||||||      |||
Db       1001 TTCACACAC---CTGGTGCAGGCCAATGTGCGCAACAAGAAGGTGTTCAAGGAAGCTGTG 1057

Qy        299 GluGluLeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGln 318
              :::   ::::::  ||||||                              ||||||
Db       1058 CAGGGCATGGTGGCCAAGGGCACCACAGGCTACAAGGCCGGCTTTGAGTATGCCTTTGAC 1117

Qy        319 IleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeu 338
                 |||:::            :::           ||||||:::   ||||||:::
Db       1118 CAGCTGCAGAACTCCAACATCACTCGGGCCAAC------TGCAACAAGATGATCATGATG 1171

Qy        339 IleSerAspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTrpProAsp 358
                 :::||||||      :::      :::   |||||||||||||||||||||||:::
Db       1172 TTCACGGATGGTGGTGAGGACCGCGTGCAGGACGTCTTTGAGAAGTACAATTGGCCAAAC 1231

Qy        359 CysLysValArgValPheThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMet 378
                 ||||||||||||||:::   :::|||:::                    :::
Db       1232 CGGACGGTGCGCGTGTTTACTTTCTCCGTGGGGCAGCATAACTATGACGTCACACCGCTG 1291

Qy        379 LysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThr 398
              :::|||:::||||||   ||||||||||||||   :::|||   ::::::
Db       1292 CAGTGGATGGCCTGTGCCAACAAAGGCTACTATTTTGAGATCCCTTCCATCGGAGCCATC 1351

Qy        399 GlnGluAsnValMetGluTyrLeuHisValLeuSerArgProMetValIle------Asn 416
              :::   |||      ||||||||||   ||||||   ||||||||||||:::
Db       1352 CGCATCAACACACAGGAATATCTAGATGTGTTGGGCAGGCCCATGGTGCTGGCAGGCAAG 1411

Qy        417 HisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGln 436
                    :::   ||||||      |||   |||
Db       1412 GAGGCCAAGCAGGTTCAGTGGACCAACGTGTATGAGGAT---------------------- 1450

Qy        437 AlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSer------------ 452
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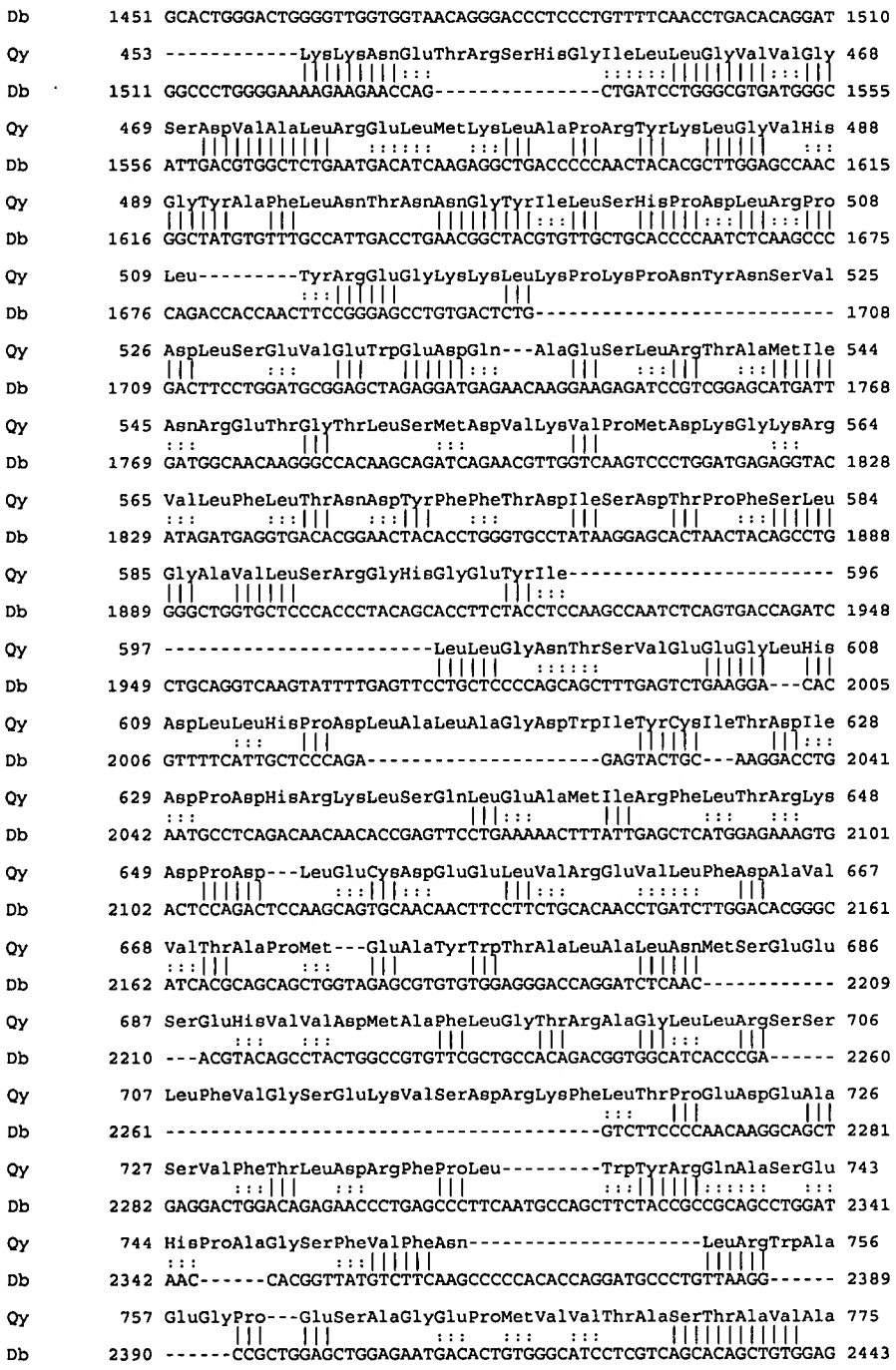

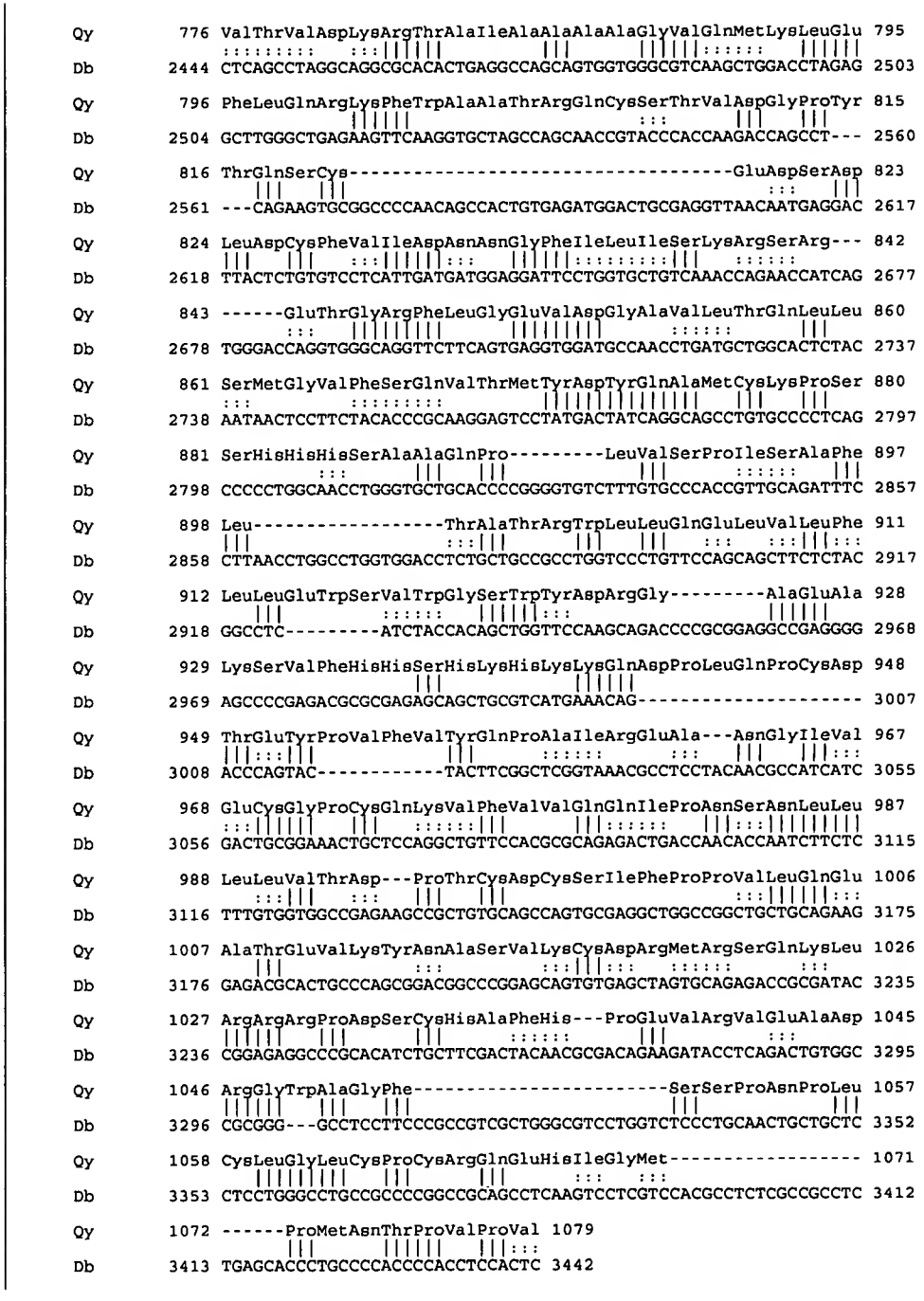

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RESULT 11
US-09-470-443-1
; Sequence 1, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
;  APPLICANT: Lerman, Michael I.
;  APPLICANT: Minna, John D.
;  APPLICANT: Latif, Farida
;  APPLICANT: Wei, Ming-Hui
;  APPLICANT: Sekido, Yoshitaka
;  APPLICANT: Gao, Boning
;  APPLICANT: Duh, Fuh-Mei
;  TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
;  FILE REFERENCE: NIH-05043
;  CURRENT APPLICATION NUMBER: US/09/470,443
;  CURRENT FILING DATE: 1999-12-22
;  EARLIER APPLICATION NUMBER: 60/114,359
;  EARLIER FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 5463
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (162)..(3599)
US-09-470-443-1

Alignment Scores:
Pred. No.:              2.26e-124      Length:          5463
Score:                  1187.50        Matches:         348
Percent Similarity:     47.59%         Conservative:    206
Best Local Similarity:  29.90%         Mismatches:      429
Query Match:            20.74%         Indels:          181
DB:                     3              Gaps:            44

US-09-833-222A-10 (1-1090) x US-09-470-443-1 (1-5463)

Qy         16 TrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeu 35
              ||||||                 ::::::        :::      :::   |||
Db        378 TGGGCCCGGCGTCTGGAGCAGGAGGTCGACGGCGTGATGCGGATTTTTGGAGGCGTCCAG 437

Qy         36 LeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55
                 |||::::::   |||||||||       :::      :::::::::|||   :::
Db        438 CAGCTCCGTGAGATTTACAAGGACAACCGGAACCTGTTCGAGGTACAGGAGAATGAGCCT 497

Qy         56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75
                 :::||||||   |||   :::   |||:::|||::::::|||  ||||||||||:::
Db        498 CAGAAGTTGGTGGAGAAGGTGGCAGGGGACATTGAGAGCCTTCTGGACAGGAAGGTGCAG 557

Qy         76 AlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
              |||::::::   |||   :::|||||||||           |||   :::   :::
Db        558 GCCCTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAAGCACACCGCTGGCAGGAC 617

Qy         96 SerLeuValPheAsp---------TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
              ::::::      :::         ||||||::::::             |||   |||:::
Db        618 AACATCAAGGAGGAAGACATCGTGTACTATGACGCCAAGGCTGACGCTGAGCTGGACGAC 677

Qy        113 ---LysGlyAsnPheValGluLeuGlyAla--------------------GluPheLeu 124
                 :::         ||||||   |||:::                   :::|||:::
Db        678 CCTGAGAGTGAGGATGTGGAAAGGGGGTCTAAGGCCAGCACCCTAAGGCTGGACTTCATC 737

Qy        125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
                 :::   |||      |||  |||      ||||||  |||   ::::::||||||
Db        738 GAGGACCCAAAC------TTCAAGAAC---AAGGTCAACTATTCATACGCGGCTGTACAG 788

Qy        145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
                 :::||||||::::::|||                |||||||||   :::      :::|||
Db        789 ATCCCTACGGACATCTACAAAGGCTCCACTGTCATCCTCAATGAGCTCAACTGGACAGAG 848

Qy        165 AlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyr 184
              ||||||      ||||||:::||||||   ::::::||||||||||||   ||||||

Db        849 GCCCTGGAGAATGTGTTCATGGAAAACCGCAGACAAGACCCCACACTGCTGTGGCAGGTC 908

Qy        185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGlu 204
              ||||||||||||||||||      |||   ||||||          |||          :::
Db        909 TTCGGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACCCCGTGGCGAGCCCCCAAG 968

Qy        205 AsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSer 224
                  :::      :::|||   |||   |||   ||||||||||||   |||:::|||
Db        969 AAG---ATCGACCTGTACGATGTCCGAAGGAGACCCTGGTATATCCAGGGGGCCTCGTCA 1025

Qy        225 ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr 244
              |||||||||:::||||||:::||||||||||||||||||:::   ||||||   :::
Db       1026 CCCAAAGACATGGTCATCATCGTGGATGTGAGTGGCAGTGTGAGCGGCCTGACCCTGAAG 1085

Qy        245 IleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsn 264
                 :::   |||   ::::::      :::||||||||||||   ::::::|||:::||||||
Db       1086 CTGATGAAGACATCTGTCTGCGAGATGCTGGACACGCTGTCTGATGATGACTATGTGAAT 1145

Qy        265 IleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
                 :::   :::::::|||:::              :::      ||||||        ||||||
Db       1146 GTGGCCTCGTTCAACGAGAAGGCACAGCCTGTGTCA---TGCTTCACACAC---CTGGTG 1199

Qy        285 GlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLys 304
              ||||||:::      |||:::::   ||||||      |||:::   ::::::   |||
Db       1200 CAGGCCAATGTGCGCAACAAGAAGGTGTTCAAGGAAGCTGTGCAGGGCATGGTGGCCAAG 1259

Qy        305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
              |||                        ||||||      |||:::
Db       1260 GGCACCACAGGCTACAAGGCCGGCTTTGAGTATGCCTTTGACCAGCTGCAGAACTCCAAC 1319

Qy        325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
                    :::                 ||||||:::   ||||||:::   :::||||||
Db       1320 ATCACTCGGGCCAAC------TGCAACAAGATGATCATGATGTTCACGGATGGTGGTGAG 1373

Qy        345 GluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLysValArgValPhe 364
              :::      :::   |||||||||||||||||||||||:::      ||||||||||||
Db       1374 GACCGCGTGCAGGACGTCTTTGAGAAGTACAATTGGCCAAACCGGACGGTGCGCGTGTTT 1433

Qy        365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn 384
              |||:::   :::|||:::                  ::::::|||:::||||||
Db       1434 ACTTTCTCCGTGGGGCAGCATAACTATGACGTCACACCGCTGCAGTGGATGGCCTGTGCC 1493

Qy        385 AsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
              ||||||||||||||   :::|||   ::::::          :::   |||      |||
Db       1494 AACAAAGGCTACTATTTTGAGATCCCTTCCATCGGAGCCATCCGCATCAACACACAGGAA 1553

Qy        405 TyrLeuHisValLeuSerArgProMetValIle------AsnHisAspHisAspIleIle 422
              ||||||  ||||||   ||||||||||||:::                        :::
Db       1554 TATCTAGATGTGTTGGGCAGGCCCATGGTGCTGGCAGGCAAGGAGGCCAAGCAGGTTCAG 1613

Qy        423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
              ||||||      |||   |||                 |||      |||   |||
Db       1614 TGGACCAACGTGTATGAGGAT--------------------GCACTGGGACTGGGGTTG 1652

Qy        443 LeuThrThrValAlaMetProValPheSer----------------------LysLys 454
                 :::   |||      :::||||||||:::                     ||||||
Db       1653 GTGGTAACAGGGACCCTCCCTGTTTTCAACCTGACACAGGATGGCCCTGGGGAAAAGAAG 1712

Qy        455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
              |||:::                 ::::::||||||||:::|||   ||||||||||||
Db       1713 AACCAG--------------CTGATCCTGGGCGTGATGGGCATTGACGTGGCTCTGAAT 1757

Qy        475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
              ::::::   :::|||   |||   |||   ||||||   :::||||||   |||
Db       1758 GACATCAAGAGGCTGACCCCCAACTACACGCTTGGAGCCAACGGCTATGTGTTTGCCATT 1817

Qy        495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu---------TyrArg 511
                    |||||||||:::|||   ||||||:::|||:::|||              :::|||
Db       1818 GACCTGAACGGCTACGTGTTGCTGCACCCCAATCTCAAGCCCCAGACCACCAACTTCCGG 1877

Qy        512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
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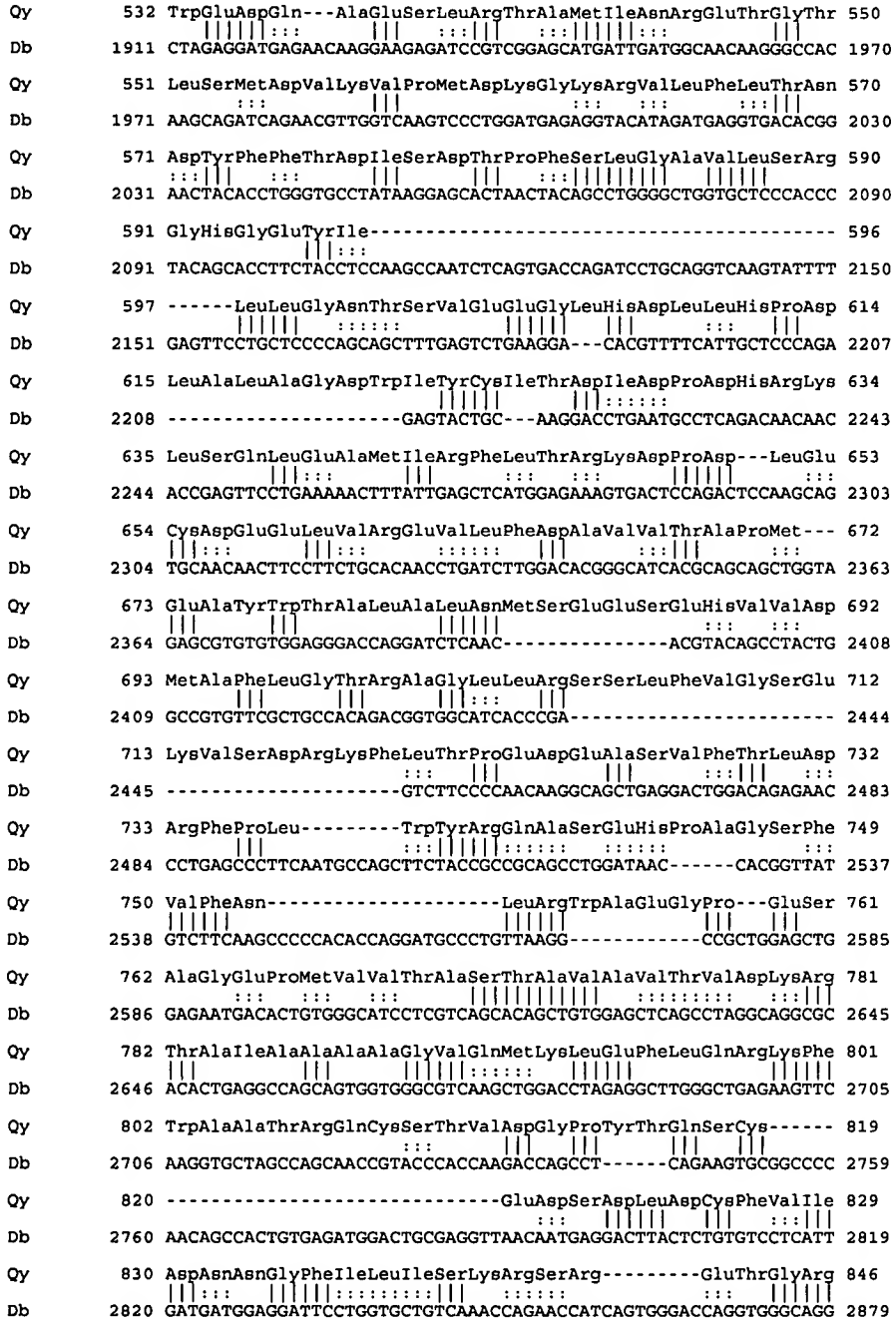

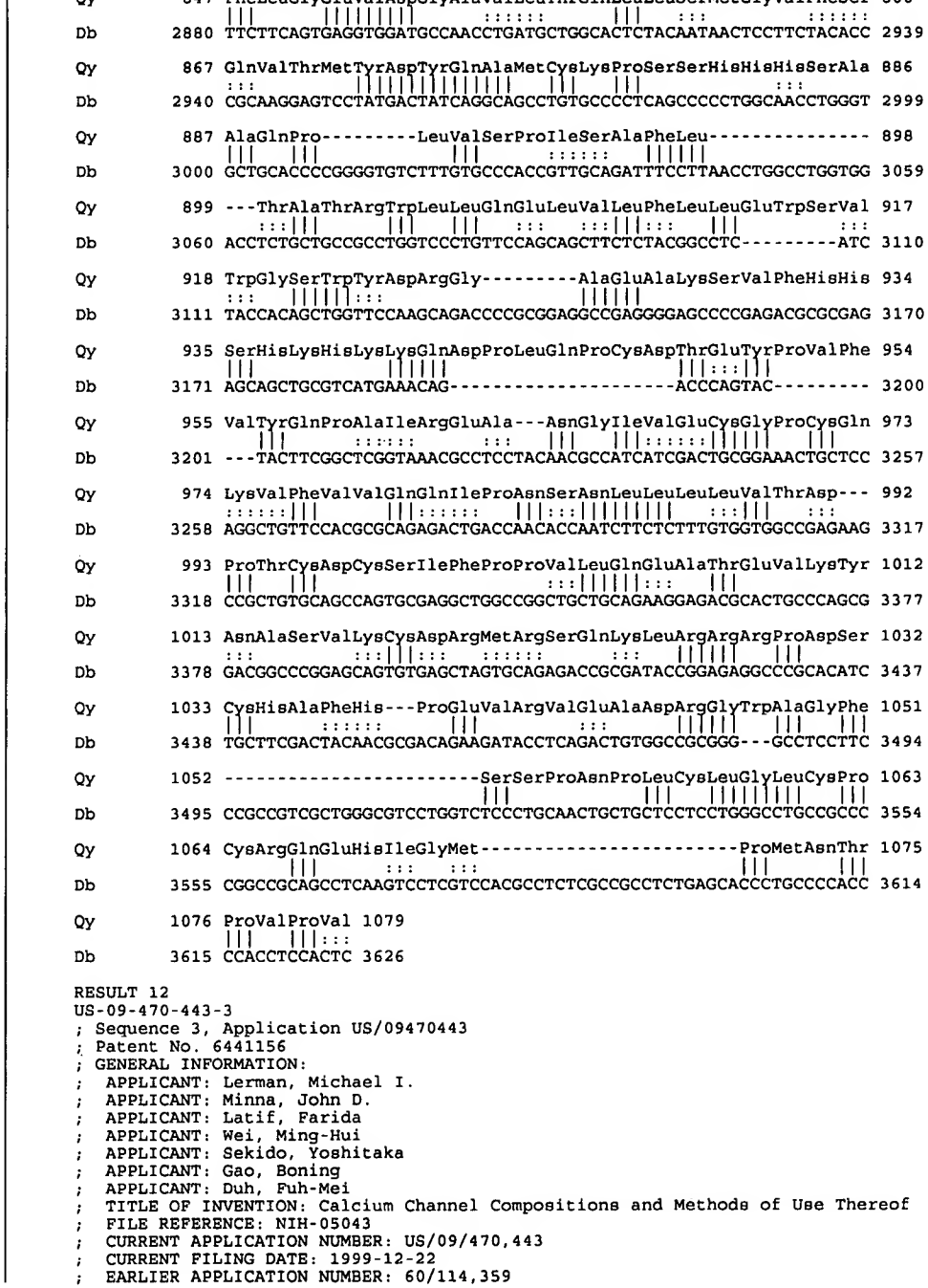

RESULT 12
US-09-470-443-3
; Sequence 3, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359

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;  EARLIER FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 5482
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (181)..(3618)
US-09-470-443-3

Alignment Scores:
Pred. No.:              2.28e-124      Length:         5482
Score:                  1187.50        Matches:        348
Percent Similarity:     47.59%         Conservative:   206
Best Local Similarity:  29.90%         Mismatches:     429
Query Match:            20.74%         Indels:         181
DB:                     3              Gaps:           44

US-09-833-222A-10 (1-1090) x US-09-470-443-3 (1-5482)

Qy         16 TrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeu 35
              ||||||              ::::::       :::     :::    |||
Db        397 TGGGCCCGGCGTCTGGAGCAGGAGGTCGACGGCGTGATGCGGATTTTTGGAGGCGTCCAG 456

Qy         36 LeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55
                 |||::::::   |||||||||      :::      :::::::::|||   :::
Db        457 CAGCTCCGTGAGATTTACAAGGACAACCGGAACCTGTTCGAGGTACAGGAGAATGAGCCT 516

Qy         56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75
                ::::::   |||   :::   |||:::|::::::|||   ||||||||:::
Db        517 CAGAAGTTGGTGGAGAAGGTGGCAGGGGACATTGAGAGCCTTCTGGACAGGAAGGTGCAG 576

Qy         76 AlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
                |||::::::   |||   :::|||||||||                |||   :::   :::
Db        577 GCCCTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAAGCACACCGCTGGCAGGAC 636

Qy         96 SerLeuValPheAsp---------TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
              ::::::      :::       ||||||::::::          |||   |||:::
Db        637 AACATCAAGGAGGAAGACATCGTGTACTATGACGCCAAGGCTGACGCTGAGCTGGACGAC 696

Qy        113 ---LysGlyAsnPheValGluLeuGlyAla--------------------GluPheLeu 124
                 :::         ||||||   |||:::                    :::|||:::
Db        697 CCTGAGAGTGAGGATGTGGAAAGGGGGTCTAAGGCCAGCACCCTAAGGCTGGACTTCATC 756

Qy        125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
                 :::   |||       |||   |||       ||||||   |||   ::::::||||||
Db        757 GAGGACCCAAAC------TTCAAGAAC---AAGGTCAACTATTCATACGCGGCTGTACAG 807

Qy        145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
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Db        808 ATCCCTACGGACATCTACAAAGGCTCCACTGTCATCCTCAATGAGCTCAACTGGACAGAG 867

Qy        165 AlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyr 184
                ||||||      ||||||:::|||||   ::::::||||||||||||   ||||||
Db        868 GCCCTGGAGAATGTGTTCATGGAAAACCGCAGACAAGACCCCACACTGCTGTGGCAGGTC 927

Qy        185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGlu 204
                |||||||||||||||||       |||   ||||||          |||          :::
Db        928 TTCGGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACCCCGTGGCGAGCCCCCAAG 987

Qy        205 AsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSer 224
                   :::     :::|||   |||   |||   ||||||||||||   |||:::|||
Db        988 AAG---ATCGACCTGTACGATGTCCGAAGGAGACCCTGGTATATCCAGGGGGCCTCGTCA 1044

Qy        225 ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr 244
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Db       1045 CCCAAAGACATGGTCATCATCGTGGATGTGAGTGGCAGTGTGAGCGGCCTGACCCTGAAG 1104

Qy        245 IleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsn 264
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Db       1105 CTGATGAAGACATCTGTCTGCGAGATGCTGGACACGCTGTCTGATGATGACTATGTGAAT 1164

Qy        265 IleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
                :::   ::::::|||:::          :::       ||||||       ||||||
Db       1165 GTGGCCTCGTTCAACGAGAAGGCACAGCCTGTGTCA---TGCTTCACACAC---CTGGTG 1218

Qy        285 GlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLys 304
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Db       1219 CAGGCCAATGTGCGCAACAAGAAGGTGTTCAAGGAAGCTGTGCAGGGCATGGTGGCCAAG 1278

Qy        305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
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Db       1279 GGCACCACAGGCTACAAGGCCGGCTTTGAGTATGCCTTTGACCAGCTGCAGAACTCCAAC 1338

Qy        325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
                   :::              ||||||:::   ||||||:::   :::|||||
Db       1339 ATCACTCGGGCCAAC------TGCAACAAGATGATCATGATGTTCACGGATGGTGGTGAG 1392

Qy        345 GluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLysValArgValPhe 364
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Db       1393 GACCGCGTGCAGGACGTCTTTGAGAAGTACAATTGGCCAAACCGGACGGTGCGCGTGTTT 1452

Qy        365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn 384
                |||:::   :::|||:::                        ::::::|||:::||||||
Db       1453 ACTTTCTCCGTGGGGCAGCATAACTATGACGTCACACCGCTGCAGTGGATGGCCTGTGCC 1512

Qy        385 AsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
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Db       1513 AACAAAGGCTACTATTTTGAGATCCCTTCCATCGGAGCCATCCGCATCAACACACAGGAA 1572

Qy        405 TyrLeuHisValLeuSerArgProMetValIle------AsnHisAspHisAspIleIle 422
                ||||||   ||||||   ||||||||||||:::                  :::
Db       1573 TATCTAGATGTGTTGGGCAGGCCCATGGTGCTGGCAGGCAAGGAGGCCAAGCAGGTTCAG 1632

Qy        423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
                ||||||      |||   |||                  |||      |||   |||
Db       1633 TGGACCAACGTGTATGAGGAT--------------------GCACTGGGACTGGGGTTG 1671

Qy        443 LeuThrThrValAlaMetProValPheSer----------------------LysLys 454
                :::   |||      :::||||||||:::                        ||||||
Db       1672 GTGGTAACAGGGACCCTCCCTGTTTTCAACCTGACACAGGATGGCCCTGGGGAAAAGAAG 1731

Qy        455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
                |||:::                :::::||||||||:::|||   ||||||||||
Db       1732 AACCAG--------------CTGATCCTGGGCGTGATGGGCATTGACGTGGCTCTGAAT 1776

Qy        475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
                ::::::   :::|||   |||   |||   ||||||   :::|||||   |||
Db       1777 GACATCAAGAGGCTGACCCCCAACTACACGCTTGGAGCCAACGGCTATGTGTTTGCCATT 1836

Qy        495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu---------TyrArg 511
                |||||||||:::|||   ||||||:::|||:::|||             :::|||
Db       1837 GACCTGAACGGCTACGTGTTGCTGCACCCCAATCTCAAGCCCCAGACCACCAACTTCCGG 1896

Qy        512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
                |||          |||                          |||      :::   |||
Db       1897 GAGCCTGTGACTCTG--------------------------GACTTCCTGGATGCGGAG 1929

Qy        532 TrpGluAspGln---AlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
                  ||||||:::      |||   :::|||   :::|||||||:::         |||
Db       1930 CTAGAGGATGAGAACAAGGAAGAGATCCGTCGGAGCATGATTGATGGCAACAAGGGCCAC 1989

Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
                   :::         |||                :::   :::      :::|||
Db       1990 AAGCAGATCAGAACGTTGGTCAAGTCCCTGGATGAGAGGTACATAGATGAGGTGACACGG 2049

Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
                :::|||   :::      |||      |||   :::|||||||||   ||||||
Db       2050 AACTACACCTGGGTGCCTATAAGGAGCACTAACTACAGCCTGGGGCTGGTGCTCCCACCC 2109

Qy        591 GlyHisGlyGluTyrIle---------------------------------------- 596
                          |||:::
Db       2110 TACAGCACCTTCTACCTCCAAGCCAATCTCAGTGACCAGATCCTGCAGGTCAAGTATTTT 2169
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Qy       597 ------LeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp 614
Db      2170 GAGTTCCTGCTCCCCAGCAGCTTTGAGTCTGAAGGA---CACGTTTTCATTGCTCCCAGA 2226

Qy       615 LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys 634
Db      2227 --------------------GAGTACTGC---AAGGACCTGAATGCCTCAGACAACAAC 2262

Qy       635 LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp---LeuGlu 653
Db      2263 ACCGAGTTCCTGAAAAACTTTATTGAGCTCATGGAGAAAGTGACTCCAGACTCCAAGCAG 2322

Qy       654 CysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet--- 672
Db      2323 TGCAACAACTTCCTTCTGCACAACCTGATCTTGGACACGGGCATCACGCAGCAGCTGGTA 2382

Qy       673 GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp 692
Db      2383 GAGCGTGTGTGGAGGGACCAGGATCTCAAC--------------ACGTACAGCCTACTG 2427

Qy       693 MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu 712
Db      2428 GCCGTGTTCGCTGCCACAGACGGTGGCATCACCCGA---------------------- 2463

Qy       713 LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp 732
Db      2464 --------------------GTCTTCCCCAACAAGGCAGCTGAGGACTGGACAGAGAAC 2502

Qy       733 ArgPheProLeu---------TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
Db      2503 CCTGAGCCCTTCAATGCCAGCTTCTACCGCCGCAGCCTGGATAAC------CACGGTTAT 2556

Qy       750 ValPheAsn--------------------LeuArgTrpAlaGluGlyPro---GluSer 761
Db      2557 GTCTTCAAGCCCCCACACCAGGATGCCCTGTTAAGG------------CCGCTGGAGCTG 2604

Qy       762 AlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLysArg 781
Db      2605 GAGAATGACACTGTGGGCATCCTCGTCAGCACAGCTGTGGAGCTCAGCCTAGGCAGGCGC 2664

Qy       782 ThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPhe 801
Db      2665 ACACTGAGGCCAGCAGTGGTGGGCGTCAAGCTGGACCTAGAGGCTTGGGCTGAGAAGTTC 2724

Qy       802 TrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys------ 819
Db      2725 AAGGTGCTAGCCAGCAACCGTACCCACCAAGACCAGCCT------CAGAAGTGCGGCCCC 2778

Qy       820 ----------------------------GluAspSerAspLeuAspCysPheValIle 829
Db      2779 AACAGCCACTGTGAGATGGACTGCGAGGTTAACAATGAGGACTTACTCTGTGTCCTCATT 2838

Qy       830 AspAsnAsnGlyPheIleLeuIleSerLysArgSerArg---------GluThrGlyArg 846
Db      2839 GATGATGGAGGATTCCTGGTGCTGTCAAACCAGAACCATCAGTGGGACCAGGTGGGCAGG 2898

Qy       847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db      2899 TTCTTCAGTGAGGTGGATGCCAACCTGATGCTGGCACTCTACAATAACTCCTTCTACACC 2958

Qy       867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla 886
Db      2959 CGCAAGGAGTCCTATGACTATCAGGCAGCCTGTGCCCCTCAGCCCCCTGGCAACCTGGGT 3018

Qy       887 AlaGlnPro---------LeuValSerProIleSerAlaPheLeu--------------- 898
Db      3019 GCTGCACCCCGGGGGTGTCTTTGTGCCCACCGTTGCAGATTTCCTTAACCTGGCCTGGTGG 3078

Qy       899 ---ThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerVal 917
Db      3079 ACCTCTGCTGCCGCCTGGTCCCTGTTCCAGCAGCTTCTCTACGGCCTC---------ATC 3129

Qy       918 TrpGlySerTrpTyrAspArgGly---------AlaGluAlaLysSerValPheHisHis 934
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Db      3130 TACCACAGCTGGTTCCAAGCAGACCCCGCGGAGGCCGAGGGGAGCCCCGAGACGCGCGAG 3189

Qy       935 SerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPhe 954
Db      3190 AGCAGCTGCGTCATGAAACAG--------------------ACCCAGTAC--------- 3219

Qy       955 ValTyrGlnProAlaIleArgGluAla---AsnGlyIleValGluCysGlyProCysGln 973
Db      3220 ---TACTTCGGCTCGGTAAACGCCTCCTACAACGCCATCATCGACTGCGGAAACTGCTCC 3276

Qy       974 LysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAsp--- 992
Db      3277 AGGCTGTTCCACGCGCAGAGACTGACCAACACCAATCTTCTCTTTGTGGTGGCCGAGAAG 3336

Qy       993 ProThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluValLysTyr 1012
Db      3337 CCGCTGTGCAGCCAGTGCGAGGCTGGCCGGCTGCTGCAGAAGGAGACGCACTGCCCAGCG 3396

Qy      1013 AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgProAspSer 1032
Db      3397 GACGGCCCGGAGCAGTGTGAGCTAGTGCAGAGACCGCGATACCGGAGAGGCCCGCACATC 3456

Qy      1033 CysHisAlaPheHis---ProGluValArgValGluAlaAspArgGlyTrpAlaGlyPhe 1051
Db      3457 TGCTTCGACTACAACGCGACAGAAGATACCTCAGACTGTGGCCGCGGG---GCCTCCTTC 3513

Qy      1052 ----------------------SerSerProAsnProLeuCysLeuGlyLeuCysPro 1063
Db      3514 CCGCCGTCGCTGGGCGTCCTGGTCTCCCTGCAACTGCTGCTCCTCCTGGGCCTGCCGCCC 3573

Qy      1064 CysArgGlnGluHisIleGlyMet----------------------ProMetAsnThr 1075
Db      3574 CGGCCGCAGCCTCAAGTCCTCGTCCACGCCTCTCGCCGCCTCTGAGCACCCTGCCCCACC 3633

Qy      1076 ProValProVal 1079
Db      3634 CCACCTCCACTC 3645
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RESULT 13
US-09-397-550-19
; Sequence 19, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 5482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-19

Alignment Scores:

Pred. No.:	2.28e-124	Length:	5482
Score:	1187.50	Matches:	348
Percent Similarity:	47.59%	Conservative:	206
Best Local Similarity:	29.90%	Mismatches:	429
Query Match:	20.74%	Indels:	181
DB:	4	Gaps:	44

US-09-833-222A-10 (1-1090) x US-09-397-550-19 (1-5482)

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Qy        16 TrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeu 35
Db       397 TGGGCCCGGCGTCTGGAGCAGGAGGTCGACGGCGTGATGCGGATTTTTGGAGGCGTCCAG 456
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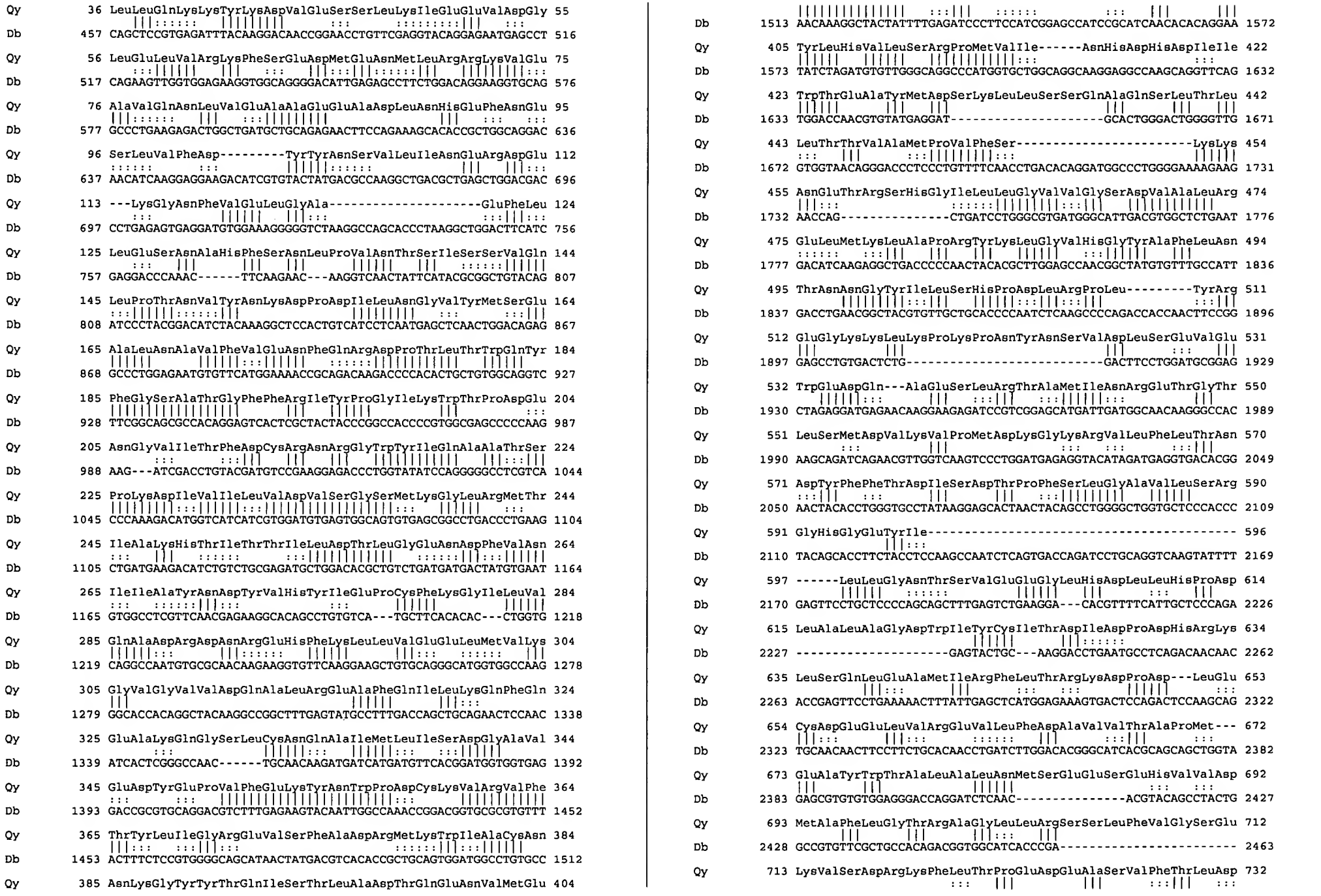

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Db       2464 --------------------GTCTTCCCCAACAAGGCAGCTGAGGACTGGACAGAGAAC 2502

Qy        733 ArgPheProLeu---------TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749

Db       2503 CCTGAGCCCTTCAATGCCAGCTTCTACCGCCGCAGCCTGGATAAC------CACGGTTAT 2556

Qy        750 ValPheAsn--------------------LeuArgTrpAlaGluGlyPro---GluSer 761

Db       2557 GTCTTCAAGCCCCCACACCAGGATGCCCTGTTAAGG-----------CCGCTGGAGCTG 2604

Qy        762 AlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLysArg 781

Db       2605 GAGAATGACACTGTGGGCATCCTCGTCAGCACAGCTGTGGAGCTCAGCCTAGGCAGGCGC 2664

Qy        782 ThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPhe 801

Db       2665 ACACTGAGGCCAGCAGTGGTGGGCGTCAAGCTGGACCTAGAGGCTTGGGCTGAGAAGTTC 2724

Qy        802 TrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys------ 819

Db       2725 AAGGTGCTAGCCAGCAACCGTACCCACCAAGACCAGCCT------CAGAAGTGCGGCCCC 2778

Qy        820 ----------------------------GluAspSerAspLeuAspCysPheValIle 829

Db       2779 AACAGCCACTGTGAGATGGACTGCGAGGTTAACAATGAGGACTTACTCTGTGTCCTCATT 2838

Qy        830 AspAsnAsnGlyPheIleLeuIleSerLysArgSerArg---------GluThrGlyArg 846

Db       2839 GATGATGGAGGATTCCTGGTGCTGTCAAACCAGAACCATCAGTGGGACCAGGTGGGCAGG 2898

Qy        847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866

Db       2899 TTCTTCAGTGAGGTGGATGCCAACCTGATGCTGGCACTCTACAATAACTCCTTCTACACC 2958

Qy        867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla 886

Db       2959 CGCAAGGAGTCCTATGACTATCAGGCAGCCTGTGCCCCTCAGCCCCCTGGCAACCTGGGT 3018

Qy        887 AlaGlnPro---------LeuValSerProIleSerAlaPheLeu-------------- 898

Db       3019 GCTGCACCCCGGGGTGTCTTTGTGCCCACCGTTGCAGATTTCCTTAACCTGGCCTGGTGG 3078

Qy        899 ---ThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerVal 917

Db       3079 ACCTCTGCTGCCGCCTGGTCCCTGTTCCAGCAGCTTCTCTACGGCCTC---------ATC 3129

Qy        918 TrpGlySerTrpTyrAspArgGly---------AlaGluAlaLysSerValPheHisHis 934

Db       3130 TACCACAGCTGGTTCCAAGCAGACCCCGCGGAGGCCGAGGGGAGCCCCGAGACGCGCGAG 3189

Qy        935 SerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPhe 954

Db       3190 AGCAGCTGCGTCATGAAACAG--------------------ACCCAGTAC--------- 3219

Qy        955 ValTyrGlnProAlaIleArgGluAla---AsnGlyIleValGluCysGlyProCysGln 973

Db       3220 ---TACTTCGGCTCGGTAAACGCCTCCTACAACGCCATCATCGACTGCGGAAACTGCTCC 3276

Qy        974 LysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAsp--- 992

Db       3277 AGGCTGTTCCACGCGCAGAGACTGACCAACACCAATCTTCTCTTTGTGGTGGCCGAGAAG 3336

Qy        993 ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr 1012

Db       3337 CCGCTGTGCAGCCAGTGCGAGGCTGGCCGGCTGCTGCAGAAGGAGACGCACTGCCCAGCG 3396

Qy       1013 AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgProAspSer 1032

Db       3397 GACGGCCCGGAGCAGTGTGAGCTAGTGCAGAGACCGCGATACCGGAGAGGCCCGCACATC 3456

Qy       1033 CysHisAlaPheHis---ProGluValArgValGluAlaAspArgGlyTrpAlaGlyPhe 1051

Db       3457 TGCTTCGACTACAACGCGACAGAAGATACCTCAGACTGTGGCCGCGGG---GCCTCCTTC 3513

Qy       1052 ------------------------SerSerProAsnProLeuCysLeuGlyLeuCysPro 1063

Db       3514 CCGCCGTCGCTGGGCGTCCTGGTCTCCCTGCAACTGCTGCTCCTCCTGGGCCTGCCGCCC 3573

Qy       1064 CysArgGlnGluHisIleGlyMet-----------------------ProMetAsnThr 1075

Db       3574 CGGCCGCAGCCTCAAGTCCTCGTCCACGCCTCTCGCCGCCTCTGAGCACCCTGCCCCACC 3633

Qy       1076 ProValProVal 1079

Db       3634 CCACCTCCACTC 3645
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RESULT 14
US-09-397-550-3
; Sequence 3, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-3

Alignment Scores:

Pred. No.:	7.63e-124	Length:	3327
Score:	1179.50	Matches:	332
Percent Similarity:	48.33%	Conservative:	202
Best Local Similarity:	30.05%	Mismatches:	408
Query Match:	20.60%	Indels:	163
DB:	4	Gaps:	40

US-09-833-222A-10 (1-1090) x US-09-397-550-3 (1-3327)

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Qy         36 LeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55

Db        277 CAGCTCCGTGAGATTTACAAGGACAACCGGAACCTGTTCGAGGTACAGGAGAATGAGCCT 336

Qy         56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75

Db        337 CAGAAGTTGGTGGAGAAGGTGGCAGGGGACATTGAGAGCCTTCTGGACAGGAAGGTGCAG 396

Qy         76 AlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95

Db        397 GCCCTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAAGCACACCGCTGGCAGGAC 456

Qy         96 SerLeuValPheAsp---------TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112

Db        457 AACATCAAGGAGGAAGACATCGTGTACTATGACGCCAAGGCTGACGCTGAGCTGGACGAC 516

Qy        113 ---LysGlyAsnPheValGluLeuGlyAla--------------------GluPheLeu 124

Db        517 CCTGAGAGTGAGGATGTGGAAAGGGGGTCTAAGGCCAGCACCCTAAGGCTGGACTTCATC 576

Qy        125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144

Db        577 GAGGACCCAAAC------TTCAAGAAC---AAGGTCAACTATTCATACGCGGCTGTACAG 627

Qy        145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
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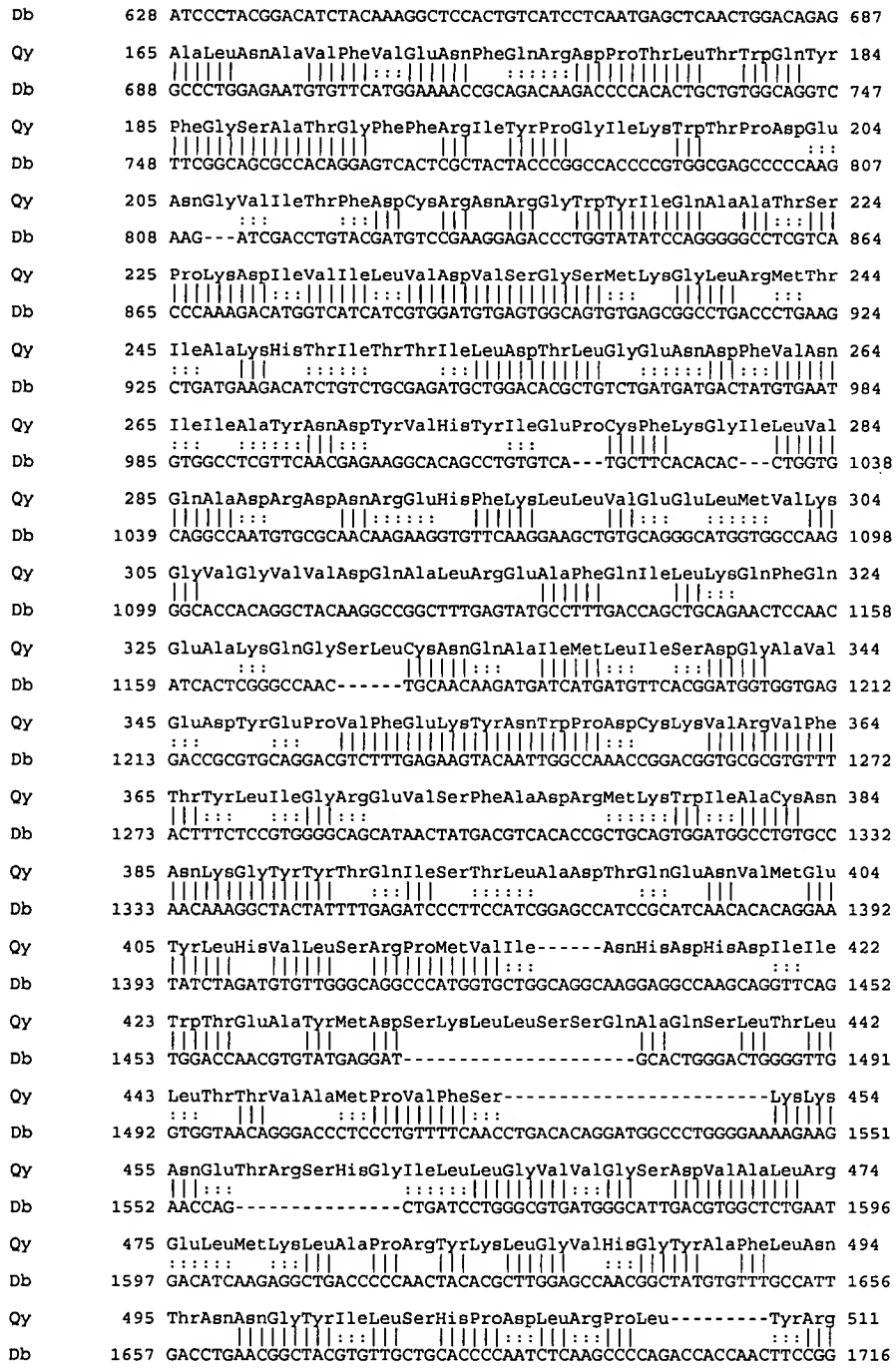
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Db 688 GCCCTGGAGAATGTGTTCATGGAAAACCGCAGACAAGACCCCACACTGCTGTGGCAGGTC 747
Qy 185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGlu 204
Db 748 TTCGGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACCCCGTGGCGAGCCCCCAAG 807
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Db 808 AAG---ATCGACCTGTACGATGTCCGAAGGAGACCCTGGTATATCCAGGGGGCCTCGTCA 864
Qy 225 ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr 244
Db 865 CCCAAAGACATGGTCATCATCGTGGATGTGAGTGGCAGTGTGAGCGGCCTGACCCTGAAG 924
Qy 245 IleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsn 264
Db 925 CTGATGAAGACATCTGTCTGCGAGATGCTGGACACGCTGTCTGATGATGACTATGTGAAT 984
Qy 265 IleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
Db 985 GTGGCCTCGTTCAACGAGAAGGCACAGCCTGTGTCA---TGCTTCACACAC---CTGGTG 1038
Qy 285 GlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLys 304
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Qy 305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
Db 1099 GGCACCACAGGCTACAAGGCCGGCTTTGAGTATGCCTTTGACCAGCTGCAGAACTCCAAC 1158
Qy 325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
Db 1159 ATCACTCGGGCCAAC------TGCAACAAGATGATCATGATGTTCACGGATGGTGGTGAG 1212
Qy 345 GluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLysValArgValPhe 364
Db 1213 GACCGCGTGCAGGACGTCTTTGAGAAGTACAATTGGCCAAACCGGACGGTGCGCGTGTTT 1272
Qy 365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn 384
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Qy 385 AsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
Db 1333 AACAAAGGCTACTATTTTGAGATCCCTTCCATCGGAGCCATCCGCATCAACACACAGGAA 1392
Qy 405 TyrLeuHisValLeuSerArgProMetValIle------AsnHisAspHisAspIleIle 422
Db 1393 TATCTAGATGTGTTGGGCAGGCCCATGGTGCTGGCAGGCAAGGAGGCCAAGCAGGTTCAG 1452
Qy 423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
Db 1453 TGGACCAACGTGTATGAGGAT--------------------GCACTGGGACTGGGGTTG 1491
Qy 443 LeuThrThrValAlaMetProValPheSer----------------------LysLys 454
Db 1492 GTGGTAACAGGGACCCTCCCTGTTTTCAACCTGACACAGGATGGCCCTGGGGAAAAGAAG 1551
Qy 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
Db 1552 AACCAG--------------CTGATCCTGGGCGTGATGGGCATTGACGTGGCTCTGAAT 1596
Qy 475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
Db 1597 GACATCAAGAGGCTGACCCCCAACTACACGCTTGGAGCCAACGGCTATGTGTTTGCCATT 1656
Qy 495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu---------TyrArg 511
Db 1657 GACCTGAACGGCTACGTGTTGCTGCACCCCAATCTCAAGCCCCAGACCACCAACTTCCGG 1716
Qy 512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
Db 1717 GAGCCTGTGACTCTG-------------------------GACTTCCTGGATGCGGAG 1749
Qy 532 TrpGluAspGln---AlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db 1750 CTAGAGGATGAGAACAAGGAAGAGATCCGTCGGAGCATGATTGATGGCAACAAGGGCCAC 1809
Qy 551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db 1810 AAGCAGATCAGAACGTTGGTCAAGTCCCTGGATGAGAGGTACATAGATGAGGTGACACGG 1869
Qy 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db 1870 AACTACACCTGGGTGCCTATAAGGAGCACTAACTACAGCCTGGGGCTGGTGCTCCCACCC 1929
Qy 591 GlyHisGlyGluTyrIle-- 596
Db 1930 TACAGCACCTTCTACCTCCAAGCCAATCTCAGTGACCAGATCCTGCAGGTCAAGTATTTT 1989
Qy 597 ------LeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp 614
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Qy 615 LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys 634
Db 2047 --------------------GAGTACTGC---AAGGACCTGAATGCCTCAGACAACAAC 2082
Qy 635 LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp---LeuGlu 653
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Qy 654 CysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet--- 672
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Qy 733 ArgPheProLeu---------TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
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Qy 750 ValPheAsn--------------------LeuArgTrpAlaGluGlyPro---GluSer 761
Db 2377 GTCTTCAAGCCCCCACACCAGGATGCCCTGTTAAGG-----------CCGCTGGAGCTG 2424
Qy 762 AlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLysArg 781
Db 2425 GAGAATGACACTGTGGGCATCCTCGTCAGCACAGCTGTGGAGCTCAGCCTAGGCAGGCGC 2484
Qy 782 ThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPhe 801
Db 2485 ACACTGAGGCCAGCAGTGGTGGGCGTCAAGCTGGACCTAGAGGCTTGGGCTGAGAAGTTC 2544
Qy 802 TrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys------ 819
Db 2545 AAGGTGCTAGCCAGCAACCGTACCCACCAAGACCAGCCT------CAGAAGTGCGGCCCC 2598
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Db 2599 AACAGCCACTGTGAGATGGACTGCGAGGTTAACAATGAGGACTTACTCTGTGTCCTCATT 2658

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Qy        830 AspAsnAsnGlyPheIleLeuIleSerLysArgSerArg---------GluThrGlyArg 846
Db       2659 GATGATGGAGGATTCCTGGTGCTGTCAAACCAGAACCATCAGTGGGACCAGGTGGGCAGG 2718

Qy        847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db       2719 TTCTTCAGTGAGGTGGATGCCAACCTGATGCTGGCACTCTACAATAACTCCTTCTACACC 2778

Qy        867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla 886
Db       2779 CGCAAGGAGTCCTATGACTATCAGGCAGCCTGTGCCCCTCAGCCCCCTGGCAACCTGGGT 2838

Qy        887 AlaGlnPro---------LeuValSerProIleSerAlaPheLeu--------------- 898
Db       2839 GCTGCACCCCGGGGTGTCTTTGTGCCCACCGTTGCAGATTTCCTTAACCTGGCCTGGTGG 2898

Qy        899 ---ThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerVal 917
Db       2899 ACCTCTGCTGCCGCCTGGTCCCTGTTCCAGCAGCTTCTCTACGGCCTC---------ATC 2949

Qy        918 TrpGlySerTrpTyrAspArgGly---------AlaGluAlaLysSerValPheHisHis 934
Db       2950 TACCACAGCTGGTTCCAAGCAGACCCCGCGGAGGCCGAGGGGAGCCCCGAGACGCGCGAG 3009

Qy        935 SerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPhe 954
Db       3010 AGCAGCTGCGTCATGAAACAG--------------------ACCCAGTAC--------- 3039

Qy        955 ValTyrGlnProAlaIleArgGluAla---AsnGlyIleValGluCysGlyProCysGln 973
Db       3040 ---TACTTCGGCTCGGTAAACGCCTCCTACAACGCCATCATCGACTGCGGAAACTGCTCC 3096

Qy        974 LysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAsp--- 992
Db       3097 AGGCTGTTCCACGCGCAGAGACTGACCAACACCAATCTTCTCTTTGTGGTGGCGAGAAG 3156

Qy        993 ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr 1012
Db       3157 CCGCTGTGCAGCCAGTGCGAGGCTGGCCGGCTGCTGCAGAAGGAGACGCACTGCCCAGCG 3216

Qy       1013 AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgProAspSer 1032
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Qy       1033 CysHisAlaPheHis 1037
Db       3277 TGCTTCGACTACAAC 3291
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RESULT 15
US-09-397-550-2
; Sequence 2, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
;  APPLICANT:  Warner-Lambert
;  TITLE OF INVENTION:  Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
;  TITLE OF INVENTION:  delta-4 calcium channel subunit polypeptides and
;  TITLE OF INVENTION:  screening assays using same
;  FILE REFERENCE:  180
;  CURRENT APPLICATION NUMBER: US/09/397,550
;  CURRENT FILING DATE:  1999-09-16
;  NUMBER OF SEQ ID NOS:  28
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 3248
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-397-550-2

Alignment Scores:
Pred. No.:              1.87e-121       Length:         3248
Score:                  1158.50         Matches:        328
Percent Similarity:     48.30%          Conservative:   197
Best Local Similarity:  30.17%          Mismatches:     399

Query Match:            20.23%          Indels:         163
DB:                     4               Gaps:           40

US-09-833-222A-10 (1-1090) x US-09-397-550-2 (1-3248)

Qy         16 TrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeu 35
Db        217 TGGGCCCGGCGTCTGGAGCAGGAGGTCGACGGCGTGATGCGGATTTTTGGAGGCGTCCAG 276

Qy         36 LeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55
Db        277 CAGCTCCGTGAGATTTACAAGGACAACCGGAACCTGTTCGAGGTACAGGAGAATGAGCCT 336

Qy         56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75
Db        337 CAGAAGTTGGTGGAGAAGGTGGCAGGGGACATTGAGAGCCTTCTGGACAGGAAGGTGCAG 396

Qy         76 AlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
Db        397 GCCCTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAAGCACACCGCTGGCAGGAC 456

Qy         96 SerLeuValPheAsp---------TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db        457 AACATCAAGGAGGAAGACATCGTGTACTATGACGCCAAGGCTGACGCTGAGCTGGACGAC 516

Qy        113 ---LysGlyAsnPheValGluLeuGlyAla--------------------GluPheLeu 124
Db        517 CCTGAGAGTGAGGATGTGGAAAGGGGGTCTAAGGCCAGCACCCTAAGGCTGGACTTCATC 576

Qy        125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
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Qy        185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGlu 204
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Qy        245 IleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsn 264
Db        925 CTGATGAAGACATCTGTCTGCGAGATGCTGGACACGCTGTCTGATGATGACTATGTGAAT 984

Qy        265 IleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
Db        985 GTGGCCTCGTTCAACGAGAAGGCACAGCCTGTGTCA---TGCTTCACACAC---CTGGTG 1038

Qy        285 GlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLys 304
Db       1039 CAGGCCAATGTGCGCAACAAGAAGGTGTTCAAGGAAGCTGTGCAGGGCATGGTGGCCAAG 1098

Qy        305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
Db       1099 GGCACCACAGGCTACAAGGCCGGCTTTGAGTATGCCTTTGACCAGCTGCAGAACTCCAAC 1158

Qy        325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
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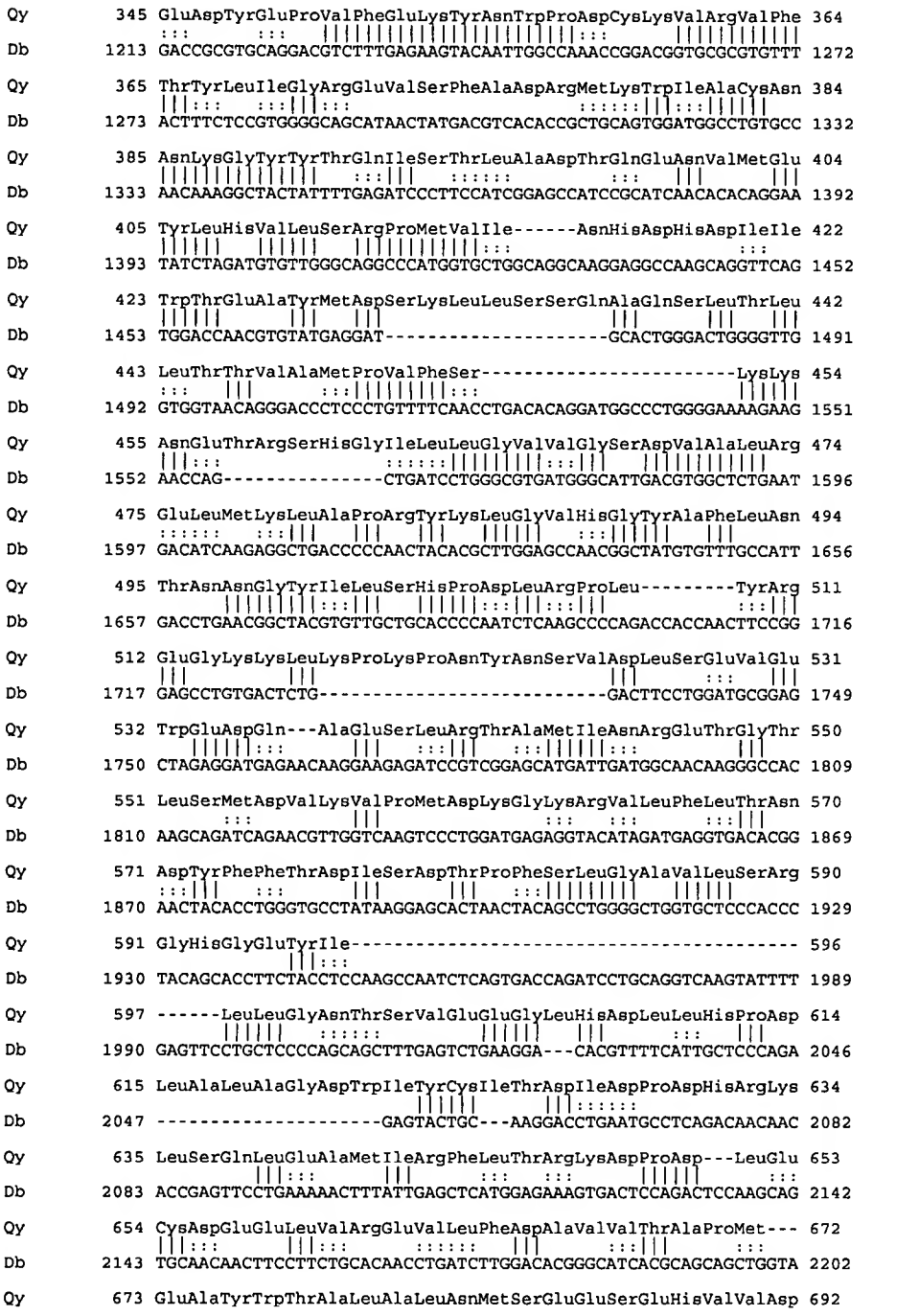
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Qy 405 TyrLeuHisValLeuSerArgProMetValIle------AsnHisAspHisAspIleIle 422
Db 1393 TATCTAGATGTGTTGGGCAGGCCCATGGTGCTGGCAGGCAAGGAGGCCAAGCAGGTTCAG 1452
Qy 423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
Db 1453 TGGACCAACGTGTATGAGGAT--------------------GCACTGGGACTGGGGTTG 1491
Qy 443 LeuThrThrValAlaMetProValPheSer----------------------LysLys 454
Db 1492 GTGGTAACAGGGACCCTCCCTGTTTTCAACCTGACACAGGATGGCCCTGGGGAAAAGAAG 1551
Qy 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
Db 1552 AACCAG--------------CTGATCCTGGGCGTGATGGGCATTGACGTGGCTCTGAAT 1596
Qy 475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
Db 1597 GACATCAAGAGGCTGACCCCCAACTACACGCTTGGAGCCAACGGCTATGTGTTTGCCATT 1656
Qy 495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu---------TyrArg 511
Db 1657 GACCTGAACGGCTACGTGTTGCTGCACCCCAATCTCAAGCCCCAGACCACCAACTTCCGG 1716
Qy 512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
Db 1717 GAGCCTGTGACTCTG--------------------------GACTTCCTGGATGCGGAG 1749
Qy 532 TrpGluAspGln---AlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db 1750 CTAGAGGATGAGAACAAGGAAGAGATCCGTCGGAGCATGATTGATGGCAACAAGGGCCAC 1809
Qy 551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db 1810 AAGCAGATCAGAACGTTGGTCAAGTCCCTGGATGAGAGGTACATAGATGAGGTGACACGG 1869
Qy 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db 1870 AACTACACCTGGGTGCCTATAAGGAGCACTAACTACAGCCTGGGGCTGGTGCTCCCACCC 1929
Qy 591 GlyHisGlyGluTyrIle-- 596
Db 1930 TACAGCACCTTCTACCTCCAAGCCAATCTCAGTGACCAGATCCTGCAGGTCAAGTATTTT 1989
Qy 597 ------LeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp 614
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Qy 615 LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys 634
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Qy 673 GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp 692
Db 2203 GAGCGTGTGTGGAGGGACCAGGATCTCAAC--------------ACGTACAGCCTACTG 2247
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Qy 713 LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp 732
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Qy 733 ArgPheProLeu---------TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
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Qy 750 ValPheAsn--------------------LeuArgTrpAlaGluGlyPro---GluSer 761
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Db 2545 AAGGTGCTAGCCAGCAACCGTACCCACCAAGACCAGCCT------CAGAAGTGCGGCCCC 2598
Qy 820 ----------------------------GluAspSerAspLeuAspCysPheValIle 829
Db 2599 AACAGCCACTGTGAGATGGACTGCGAGGTTAACAATGAGGACTTACTCTGTGTCCTCATT 2658
Qy 830 AspAsnAsnGlyPheIleLeuIleSerLysArgSerArg---------GluThrGlyArg 846
Db 2659 GATGATGGAGGATTCCTGGTGCTGTCAAACCAGAACCATCAGTGGGACCAGGTGGGCAGG 2718
Qy 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db 2719 TTCTTCAGTGAGGTGGATGCCAACCTGATGCTGGCACTCTACAATAACTCCTTCTACACC 2778
Qy 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla 886
Db 2779 CGCAAGGAGTCCTATGACTATCAGGCAGCCTGTGCCCCTCAGCCCCCTGGCAACCTGGGT 2838
Qy 887 AlaGlnPro---------LeuValSerProIleSerAlaPheLeu---------------- 898
Db 2839 GCTGCACCCCGGGGTGTCTTTGTGCCCACCGTTGCAGATTTCCTTAACCTGGCCTGGTGG 2898
Qy 899 ---ThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerVal 917
Db 2899 ACCTCTGCTGCCGCCTGGTCCCTGTTCCAGCAGCTTCTCTACGGCCTC---------ATC 2949
Qy 918 TrpGlySerTrpTyrAspArgGly---------AlaGluAlaLysSerValPheHisHis 934
Db 2950 TACCACAGCTGGTTCCAAGCAGACCCCGCGGAGGCCGAGGGGAGCCCCGAGACGCGCGAG 3009
Qy 935 SerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPhe 954
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Qy 955 ValTyrGlnProAlaIleArgGluAla---AsnGlyIleValGluCysGlyProCysGln 973
Db 3040 ---TACTTCGGCTCGGTAAACGCCTCCTACAACGCCATCATCGACTGCGGAAACTGCTCC 3096
Qy 974 LysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAsp--- 992
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Qy 993 ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr 1012

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Db       3157 CCGCTGTGCAGCCAGTGCGAGGCTGGCCGGCTGCTGCAGAAGGAGACGCACTGCCCAGCG 3216

Qy       1013 AsnAlaSerValLysCysAsp 1019
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Db       3217 GACGGCCCGGAGCAGTGTGAG 3237
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Search completed: November 17, 2005, 05:42:12
Job time : 602 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2005, 22:05:05 ; Search time 8018 Seconds
(without alignments)
5174.614 Million cell updates/sec

Title: US-09-833-222A-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTPVPVLLGGNIRVYAL 1090

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US09833222/runat_15112005_145358_15791/app_query.fasta_1.1287
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09833222_@CGN_1_1_4804_@runat_15112005_145358_15791 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2593.5	45.3	2730	9	AY404364	AY404364 Homo sapi
2	2591	45.2	2690	9	AY404366	AY404366 Mus muscu
3	2493.5	43.5	2730	9	AY404365	AY404365 Pan trogl
4	2241	39.1	2583	3	AK030723	AK030723 Mus muscu
5	1800.5	31.4	3230	3	AK044427	AK044427 Mus muscu
6	1356	23.7	916	4	BI518624	BI518624 603061574
7	1317.5	23.0	892	1	AL558158	AL558158 AL558158
8	1297	22.7	1446	3	CR603629	CR603629 full-leng
c 9	1266	22.1	747	6	CD743170	CD743170 UI-H-FT1-
10	1246.5	21.8	853	4	BI908421	BI908421 603067367
11	1228	21.4	765	7	CO424223	CO424223 UI-M-HU0-
12	1208	21.1	940	5	BQ919363	BQ919363 AGENCOURT
13	1182.5	20.7	777	4	BI908463	BI908463 603069223
14	1180	20.6	3527	3	AK044603	AK044603 Mus muscu
15	1157.5	20.2	725	4	BG436760	BG436760 602489181
16	1136	19.8	942	5	BU155034	BU155034 AGENCOURT
17	1130	19.7	776	7	CN539658	CN539658 UI-M-HU0-
18	1107	19.3	764	4	BI906089	BI906089 603062468
19	1092.5	19.1	946	5	BU749673	BU749673 CH3#028_C
20	1063	18.6	656	4	BM009121	BM009121 603629489
21	1030	18.0	651	2	BB278653	BB278653 BB278653
22	1029	18.0	893	6	CD513443	CD513443 AGENCOURT
23	985.5	17.2	3675	3	AK014825	AK014825 Mus muscu
24	974	17.0	842	6	CD107126	CD107126 AGENCOURT
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26	936.5	16.4	601	2	BE276523	BE276523 601144143
27	931	16.3	794	7	CK130243	CK130243 AGENCOURT
c 28	928.5	16.2	816	7	CN076590	CN076590 EC2BBA12A
29	927	16.2	779	7	CK130239	CK130239 AGENCOURT
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31	910	15.9	753	7	CK130241	CK130241 AGENCOURT
32	901.5	15.7	2791	9	AY403434	AY403434 Homo sapi
c 33	898.5	15.7	852	5	BX329163	BX329163 BX329163
34	897.5	15.7	2730	9	AY403436	AY403436 Mus muscu
35	894	15.6	713	7	CK130240	CK130240 AGENCOURT
36	873	15.2	818	2	BE740459	BE740459 601595508
37	866	15.1	819	5	BU747580	BU747580 CH3#013_G
38	854	14.9	498	5	BQ636196	BQ636196 hd05g08.y
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c 41	817.5	14.3	806	5	BU749672	BU749672 CH3#028_C
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44	794.5	13.9	526	2	AW656595	AW656595 108929 MA
45	790.5	13.8	522	2	AW656606	AW656606 108945 MA

ALIGNMENTS

RESULT 1
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DEFINITION Homo sapiens CACNA2D3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY404364
VERSION AY404364.1 GI:39760341
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2730)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2730)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .2730

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                     /locus_tag="HCM1866"
ORIGIN

Alignment Scores:
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Score:                    2593.50        Matches:         487
Percent Similarity:       70.78%         Conservative:    155
Best Local Similarity:    53.69%         Mismatches:      248
Query Match:              45.29%         Indels:          18
DB:                       9              Gaps:            7

US-09-833-222A-10 (1-1090) x AY404364 (1-2730)

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Qy        174 PheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArg 193
Db         61 TTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTTTTTAGG 120

Qy        194 IleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCysArg 213
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Qy        214 AsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuValAsp 233
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Qy        234 ValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThrIle 253
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Qy        274 TyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGluHis 293
Db        361 TATGTGGAACCTTGCCTGAATGGAACTTTGGTGCAAGCCGACAGGACAAACAAAGAGCAC 420

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Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
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Db       1021 GCCTTTGCAATCACAAATAATGGATATATCCTGACGCATCCGGAACTCAGGCTGCTGTAC 1080

Qy        511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
Db       1081 GAAGAAGGAAAAAAG---CGAAGGAAACCTAACTATAGTAGCGTTGACCTCTCTGAGGTG 1137

Qy        531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db       1138 GAGTGGGAAGACCGAGATGACGTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1197

Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db       1198 NNNNCCATGGAGGTGAAGAAGACAGTGGACAAAGGGAAACGGGTTTTGGTGATGACAAAT 1257

Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db       1258 GACTACTATTATACAGACATCAAGGGTACTCCTTTCAGTTTAGGTGTGGCGCTTTCCAGA 1317

Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db       1318 GGTCATGGGAAATATTTCTTCCGAGGGAATGTAACCATCGAAGAAGGCCTGCATGACTTA 1377

Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db       1378 GAACATCCCGATGTGTCCTTGGCAGATGAATGGTCCTACTGCAACACTGACCTACACCCT 1437

Qy        631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db       1438 GAGCACCGCCATCTGTCTCAGTTAGAAGCGATTAAGCTCTACCTAAAAGGCAAAGAACCT 1497

Qy        651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db       1498 CTGCTCCAGTGTGATAAAGAATTGATCCAAGAAGTCCTTTTTGACGCGGTGGTGAGTGCC 1557

Qy        671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db       1558 CCCATTGAAGCGTATTGGACCAGCCTGGCCCTCAACAAATCTGAAAATTCTGACAAGGGC 1617

Qy        691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
Db       1618 GTGGAGGTTGCCTTCCTCGGCACTCGCACGGGCCTCTCCAGAATCAACCTGTTTGTCGGG 1677

Qy        711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
Db       1678 GCTGAGCAGCTCACCAATCAGGACTTCCTGAAAGCTGGCGACAAGGAGAACATTTTTAAC 1737

Qy        731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750
Db       1738 GCAGACCATTTCCCTCTCTGGTACCGAAGAGCCGCTGAGCAGATTCCAGGGAGCTTCGTC 1797

Qy        751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
Db       1798 TACTCGATCCCATTCAGCACTGGACCA------GTCAATAAAAGCAATGTGGTGACAGCA 1851

Qy        771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyVal 790
Db       1852 AGTACATCCATCCAGCTCCTGGATGAACGGAAATCTCCTGTGGTGGCAGCTGTAGGCATT 1911
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Qy        791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
              ||||||||||||||||||  ||||||||||||||   |||:::|||||||||:::::: 
Db       1912 CAGATGAAACTTGAATTTTTCCAAAGGAAGTTCTGGACTGCCAGCAGACAGTGTGCTTCC 1971

Qy        811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
              :::||||||      :::   ||||||:::|||      ::::::|||::::::|||||| 
Db       1972 CTGGATGGCAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTGTTACCTCATAGAC 2031

Qy        831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
              ||||||||||||||||||:::|||:::          :::||||||   |||   |||||| 
Db       2032 AATAATGGATTTATTTTGGTGTCTGAAGACTACACACAGACTGGAGACTTTTTTGGTGAG 2091

Qy        851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
              ::::::|||||||||:::   :::||||||:::||||||   |||   ::::::|||::: 
Db       2092 ATCGAGGGAGCTGTGATGAACAAATTGCTAACAATGGGCTCCTTTAAAAGAATTACCCTT 2151

Qy        871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890
              ||||||||||||||||||:::   :::                |||       ||| 
Db       2152 TATGACTACCAAGCCATGTGTAGAGCCAACAAGGAAAGCAGCGATGGCGCCCATGGCCTC 2211

Qy        891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910
              :::   |||   :::|||||||||:::|||   :::|||::::::   |||||||||||| 
Db       2212 CTGGATCCTTATAATGCCTTCCTCTCTGCAGTAAAATGGATCATGACAGAACTTGTCTTG 2271

Qy        911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
              ||||||:::|||:::::::::      ||||||:::                ||||||::: 
Db       2272 TTCCTGGTGGAATTTAACCTCTGC---AGTTGGTGGCACTCCGATATGACAGCTAAAGCC 2328

Qy        931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
                                     |||   :::      |||:::|||||||||||||| 
Db       2329 --------------------CAGAAATTGAAACAGACCCTGGAGCCTTGTGATACTGAA 2367

Qy        951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
              ||||||  ||||||  :::      |||:::|||      |||   :::   ||| 
Db       2368 TATCCAGCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGGAATATTGCTTGTGAA 2427

Qy        971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990
                 |||   |||   ||||||:::||||||||||||:::|||||||||   ::::::||| 
Db       2428 GACTGCTCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAACCTGTTCATGGTGGTG 2487

Qy        991 ThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010
                 |||   :::|||   |||              |||:::                 |||::: 
Db       2488 GTGGACAGCAGCTGCCTCTGTGAATCTGTGGCCCCCATCACCATGGCACCCATTGAAATC 2547

Qy       1011 ---LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArg 1029
                 ::::::|||   |||:::||||||:::|||:::::::::||||||:::|||||||||| 
Db       2548 AGTCAACATAATGAATCCCTTAAGTGTGAACGTCTAAAGGCCCAGAAGATCAGAAGGCGC 2607

Qy       1030 ProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
              |||:::|||||||||   ||||||||||||              |||         ||| 
Db       2608 CCAGAATCTTGTCATGGCTTCCATCCTGAG------GAGAATGCAAGGGAGTG-TGGGGG 2660

Qy       1050 GlyPheSerSerProAsnPro 1056
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Db       2661 TGCGCCGAGTCTCCAAGCCCA 2681
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RESULT 2
AY404366
LOCUS       AY404366               2690 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus CACNA2D3 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY404366
VERSION     AY404366.1  GI:39760343
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2690)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2690)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2690
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>2690
                     /gene="CACNA2D3"
                     /locus_tag="HCM1866"
ORIGIN
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Pred. No.:                9.74e-270      Length:          2690
Score:                    2591.00        Matches:         490
Percent Similarity:       70.49%         Conservative:    155
Best Local Similarity:    53.55%         Mismatches:      239
Query Match:              45.25%         Indels:          32
DB:                       9              Gaps:            8

US-09-833-222A-10 (1-1090) x AY404366 (1-2690)

Qy        154 ProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGluAsn 173
              |||   |||:::|||||||||||||   ||||||:::||||||   ||||||||||:::||| 
Db          1 CCTGCCATTGTCAATGGAGTGTATTGGTCTGAATCTCTAAACAAAGTTTTTGTGGATAAC 60

Qy        174 PheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArg 193
              |||   ||||||||:::|||   ||||||||||||||||||||   |||||||||||| 
Db         61 TTTGATCGGGATCCGTCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTTTTCAGA 120

Qy        194 IleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCysArg 213
                 ||||||||||||||||   ||||||||||||||||||||   ||||||||||| 
Db        121 CAGTACCCAGGGATTAAATGGGAACCAGATGAGAATGGAGTCATTGCCTTTGACTGCAGG 180

Qy        214 AsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuValAsp 233
              ||||||   ||||||||||||||||||||||||||||||:::|||||||||||||||| 
Db        181 AACAGAAAATGGTACATCCAGGCAGCGACTTCTCCAAAGGATGTTGTCATTTTGGTGGAC 240

Qy        234 ValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThrIle 253
              |||||||||||||||||||||||||||||:::|||||||||||   |||:::::::::|| 
Db        241 GTCAGTGGGAGCATGAAAGGACTCCGCTTGACCATCGCCAAGCAAACAGTGTCCTCAATA 300

Qy        254 LeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrValHis 273
              ||||||||||||||:::::||||||   |||||||||   ||||||:::   :::||| 
Db        301 CTGGATACTCTGGGTGATGATGACTTCTTCAACATCATCACGTATAACGAAGAGCTTCAC 360

Qy        274 TyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGluHis 293
              |||:::|||||||||      |||   ||||||||||||||||   |||:::|||||| 
Db        361 TATGTGGAACCTTGTCTGAACGGAACACTGGTTCAAGCTGACAGGACCAACAAGGAGCAC 420

Qy        294 PheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAlaLeu 313
              |||:::      :::::::::|||      ||||||:::|||::::::|||   ||||||
Db        421 TTCAGGGAGCATTTGGACAAACTTTTTGCCAAAGGGATTGGAATGCTGGATATCGCACTG 480

Qy        314 ArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsn 333
                 |||||||||   ||||||
Db        481 AACGAGGCCTTCAACATACTGAGCGATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 540

Qy        334 GlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGluLys 353

Db        541 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 600
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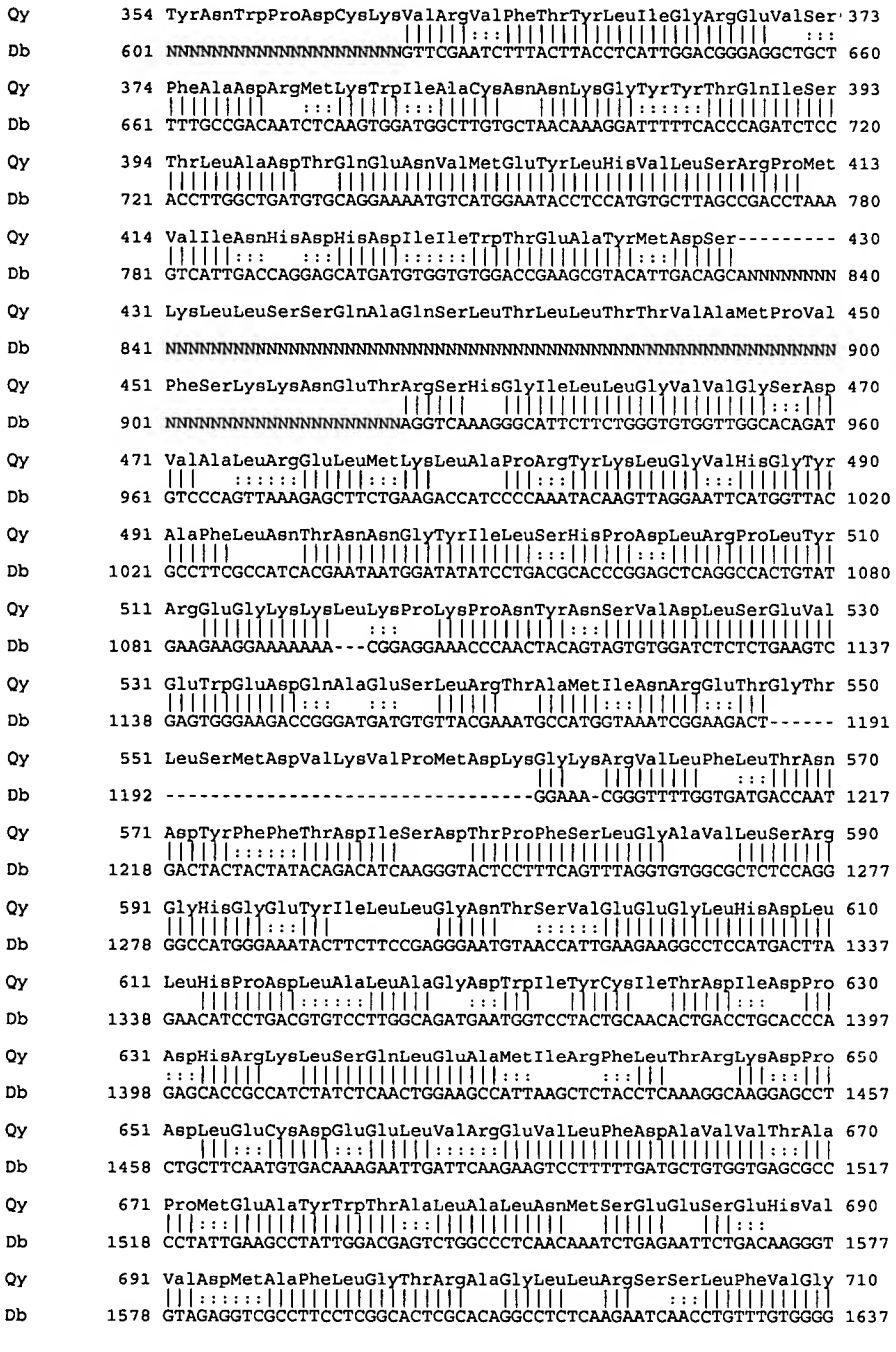

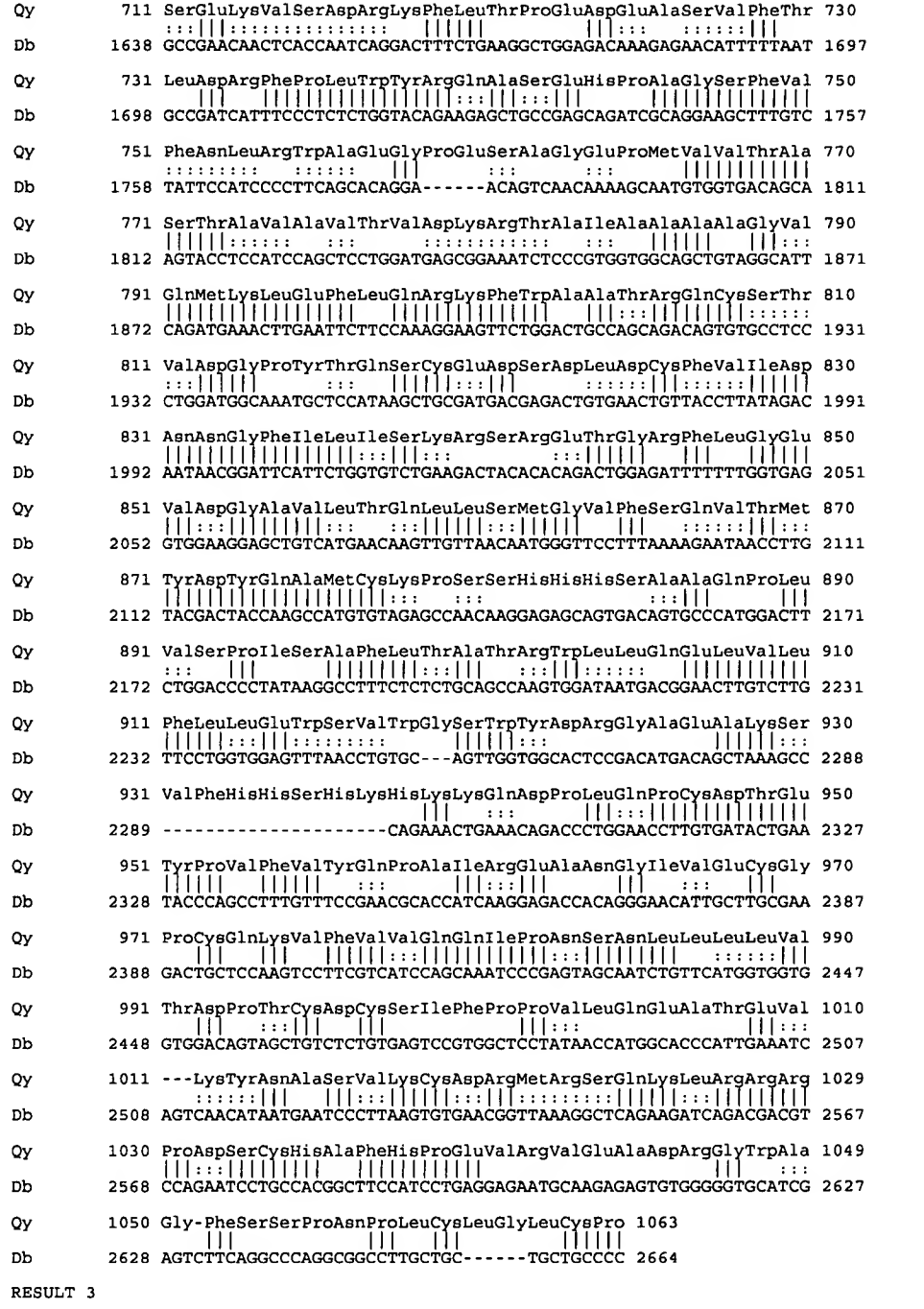

RESULT 3

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AY404365
LOCUS       AY404365               2730 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Pan troglodytes CACNA2D3 gene, VIRTUAL TRANSCRIPT, partial
            sequence, genomic survey sequence.
ACCESSION   AY404365
VERSION     AY404365.1  GI:39760342
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 2730)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2730)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2730
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>2730
                     /gene="CACNA2D3"
                     /locus_tag="HCM1866"
ORIGIN

Alignment Scores:
Pred. No.:                4.1e-259      Length:          2730
Score:                    2493.50       Matches:         473
Percent Similarity:       68.25%        Conservative:    146
Best Local Similarity:    52.15%        Mismatches:      271
Query Match:              43.55%        Indels:          18
DB:                       9             Gaps:            7

US-09-833-222A-10 (1-1090) x AY404365 (1-2730)

Qy        154 ProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGluAsn 173
              |||  |||:::|||||||||||||  ||||||::||||||  |||||||||:::|||
Db          1 CCTGCAATTGTCAATGGGGTTTATTGGTCTGAATCTCTAAACAAAGTTTTTGTAGATAAC 60

Qy        174 PheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArg 193
              |||  |||||||||:::|||  ||||||||||||||||||||  ||||||||||||
Db         61 TTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGAAGTGCAAAGGGCTTTTTTAGG 120

Qy        194 IleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCysArg 213
              ||||||||||||||||||  ||||||||||||||||||||  ||||||||||||
Db        121 CAGTATCCGGGGATTAAATGGGAACCAGATGAGAATGGAGTCATTGCCTTCGACTGCAGG 180

Qy        214 AsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuValAsp 233
              ||||||  ||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        181 AACCGAAAATGGTACATCCAGGCAGCAACTTCTCCGAAAGACGTGGTCATTTTAGTTGAC 240

Qy        234 ValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThrIle 253
              ||||||||||||||||||||||||||:::||||||||||  |||||||||||||
Db        241 GTCAGTGGCAGCATGAAAGGACTCCGTCTGACTATCGCGAAGCAAACAGTCTCATCCATT 300

Qy        254 LeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrValHis 273
              ||||||||||||||:::::||||||  ||||||||||||||||:::  :::|||
Db        301 TTGGATACACTTGGGGATGATGACTTCTTCAACATAATTGCTTATAATGAGGAGCTTCAC 360

Qy        274 TyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGluHis 293
              |||:::|||||||||  |||  ||||||||||||||||||  |||:::|||||||
Db        361 TATGTGGAACCTTGCCTGAATGGAACTTTGGTGCAAGCCGACAGGACAAACAAAGAGCAC 420

Qy        294 PheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAlaLeu 313
              |||:::  :::::::::|||  ||||||:::|||::::::|||  ||||||
Db        421 TTCAGGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTGGAATGTTGGATATAGCTTTG 480

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              |||||||||  ||||||
Db        481 AATGAGGCCTTCAACATTCTGAGTGATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 540

Qy        334 GlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGluLys 353

Db        541 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 600

Qy        354 TyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluValSer 373
                                  ||||||:::|||||||||||||||||||||||||  :::
Db        601 NNNNNNNNNNNNNNNNNNNNGTTCGCATCTTCACATACCTCATTGGACGAGAGGCTGCG 660

Qy        374 PheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIleSer 393
              |||||||||  :::||||||:::||||||  |||||||||::::::|||||||||||||
Db        661 TTTGCAGACAATCTAAAGTGGATGGCCTGTGCCAACAAAGGATTTTTTACCCAGATCTCC 720

Qy        394 ThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgProMet 413
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTGGCTGATGTGCAGGAGAATGTCATGGAATACCTTCACGTGCTTAGCCGGCCCAAA 780

Qy        414 ValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer--------- 430
              ||||||:::  :::|||||||::::::|||||||||||||||:::|||||||
Db        781 GTCATCGACCAGGAGCATGATGTGGTGTGGACCGAAGCTTACATTGACAGCANNNNNNNN 840

Qy        431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450

Db        841 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 900

Qy        451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
                                  ||||||  ||||||||||||||||||||||||:::|||
Db        901 NNNNNNNNNNNNNNNNNNNNAGATCGAAGGGCATTCTTCTGGGAGTGGTTGGCACAGAT 960

Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
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Db        961 GTCCCAGTCAAAGAACTTCTGAAGACCATCCCCAAATACAAGTTAGGGATTCACGGTTAT 1020

Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
              ||||||  ||||||||||||||||||||:::||||||:::||||||  ||||||
Db       1021 GCCTTTGCAATCACAAATAATGGATATATCCTGACGCATCCGGAACTCAGGCTGCTGTAC 1080

Qy        511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
                ||||||||||||  :::  ||||||||||||:::|||||||||||||||||||||
Db       1081 GAAGAAGGAAAAAAG---CGAAGGAAACCTAACTATAGTAGCGTTGACCTCTCTGAGGTG 1137

Qy        531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
              ||||||||||||:::  :::
Db       1138 GAGTGGGAAGACCGAGATGACGTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1197

Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
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Db       1198 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAACGGGTTTTGGTGATGACAAAT 1257

Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
              ||||||::::::|||||||||  ||||||||||||||||||  |||||||||
Db       1258 GACTACTATTATACAGACATCAAGGGTACTCCTTTCAGTTTAGGTGTGGCGCTTTCCAGA 1317

Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
              |||||||||:::|||  ||||||  ::::::|||||||||||||||||||||||||||
Db       1318 GGTCATGGGAAATATTNNTTCCGAGGGAATGTAACCATCGAAGAAGGCCTGCATGACTTA 1377

Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
                |||||||||::::::||||||  :::|||  ||||||  ||||||:::  |||
Db       1378 GAACATCCCGATGTGTCCTTGGCAGATGAATGGTCCTACTGCAACACTGACCTACACCCT 1437
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Qy       631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db      1438 GAGCACCGCCATCTGTCTCAGTTAGAANCGATTAAGCTCTACCTAAAAGGCAAAGAACCT 1497

Qy       651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db      1498 CTGCTCCAGTGTGATAAAGAATTGATCCAAGAAGTCCTTTTTGACGCGGTGGTGAGTGCC 1557

Qy       671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db      1558 CCCATTGAAGCGTATTGGACCAGCCTGGCCCTCAACAAATCTGANNNNNNNNNCAAGGGC 1617

Qy       691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
Db      1618 GTGGAGGTTGCCTTNNNNNGCACTCGCACGGGCNNNNNCAGAATCAACCTGTTTGTCGGG 1677

Qy       711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
Db      1678 GNNNNNNNNNNNNNNNNNNGGACTTCCTGAAAGCTGGCGACAAGGAGAACATTTTTAAC 1737

Qy       731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750
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Qy       751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
Db      1798 TACTCGATCCCGTTCAGCACTGGACCA------GTCAATAAAAGCAATGTGGTGACAGCG 1851

Qy       771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyVal 790
Db      1852 AGTACATCCATCCAGCTCCTGGATGAACGGAAATCTCCTGTGGTGGCAGCTGTAGGCATT 1911

Qy       791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
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Qy       811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
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Qy       831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db      2032 AATAATGGATTTATTTTGGTGTCTGAAGACTACACACAGACTGGAGACTTTTTGGTGAG 2091

Qy       851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
Db      2092 ATCGAGGGAGCTGTGATGAACAAATTGCTAACAATGGGCTCCTTTAAAAGAATTACCCTT 2151

Qy       871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890
Db      2152 TATGACTACCAAGCCATGTGTAGAGCCAACAAGGAAAGCAGCGATGGCGCCCATGGCCTC 2211

Qy       891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910
Db      2212 CTGGATCCTTATAATGCCTTCCTCTCTGCAGTAAAATGGATCATGACAGAACTTGTCTTG 2271

Qy       911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
Db      2272 TTCCTGGTGGAATTTAACCTCTGC---AGTTGGTGGCACTCCGATATGACAGCTAAAGCC 2328

Qy       931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
Db      2329 --------------------CAGAAATTGAAACAGACCCTGGAGCCTTGTGATACTGAA 2367

Qy       951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
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Qy       971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990
Db      2428 GACTGCTCCAAGTCCTTTGTCATCCAGCAAATCCCAAGCAGCAACCTGTTCATGGTGGTG 2487

Qy       991 ThrAspProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluVal 1010

                                                                          
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Qy      1011 ---LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArg 1029
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Qy      1030 ProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
Db      2608 CCAGAATCTTGTCATGGCTTCCATCCTGAG------GAGAATGCAAGGGAGTG-TGGGGG 2660

Qy      1050 GlyPheSerSerProAsnPro 1056
Db      2661 TGCACCGAGTCTCCAAGCCCA 2681
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RESULT 4
AK030723

LOCUS	AK030723 2583 bp mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730412N02 product:hypothetical von Willebrand factor type A domain containing protein, full insert sequence.
ACCESSION	AK030723
VERSION	AK030723.1 GI:26081962
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2583)
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

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            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
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                     /tissue_type="whole body"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="8 days embryo"
     misc_feature    1. .2583
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                     containing protein (InterPro|IPR002035, evidence:
                     InterPro)"
ORIGIN

Alignment Scores:
Pred. No.:              1.14e-231      Length:          2583
Score:                  2241.00        Matches:         422
Percent Similarity:     95.64%         Conservative:    17
Best Local Similarity:  91.94%         Mismatches:      20
Query Match:            39.14%         Indels:          0
DB:                     3              Gaps:            0

US-09-833-222A-10 (1-1090) x AK030723 (1-2583)

Qy        197 GlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGly 216
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Db        215 GGAATAAAGTGGATGCCTGATGAAAACGGAGTCATCGCCTTCGACTGCAGAAACCGTGGC 274

Qy        217 TrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuValAspValSerGly 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        275 TGGTACATACAAGCTGCCACATCTCCCAAAGACATCGTAATTCTGGTGGACATTAGCGGC 334

Qy        237 SerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThrIleLeuAspThr 256
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        335 AGCATGAAGGGGCTGAGGATGGCTATCGCCAAGCACACCATTACCACCATATTGGACACC 394

Qy        257 LeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrValHisTyrIleGlu 276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 CTGGGAGAGAACGACTTCGTGAACATCATCGCGTACAATGACTACGTCCACTACATTGAG 454

Qy        277 ProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGluHisPheLysLeu 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 CCCTGCTTCAAAGGCATCCTTGTCCAAGCAGATCGAGACAACCGAGAGCATTTCAAGCAG 514

Qy        297 LeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAla 316
              ||||||:::||||||||||||||||||||||||||||||   |||||||||   ||||||
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Qy        317 PheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIle 336
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Db        575 TTCGAGATCCTGAAACAGTTCCAAGAGTCCAAACAAGGAAGTCTCTGCAACCAGGCCATC 634

Qy        337 MetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTrp 356
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Qy        357 ProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluValSerPheAlaAsp 376
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Db        755 CGCATGAAGTGGATCGCCTGCAACAATAAAGGCTACTACACACAGATCTCCACACTGGCG 814

Qy        397 AspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgProMetValIleAsn 416
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Db        815 GATGCGCAGGAGAGCGTGATGGAGTACCTGCATGTGCTTAGCCGCCCCATGGTCATCAAC 874

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Qy        437 AlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSerLysLysAsnGlu 456
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Db        935 GCACAGAGCCTGATGCTCCTCACCACAGTGGCCATGCCTGTCTTCAGCAAAAAGAATGAA 994

Qy        457 ThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeu 476
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Qy        477 MetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsnThrAsn 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1055 ATGAAGCTGGCACCCCGATATAAGCTTGGGGTGCATGGCTATGCCTTCTTGAACACTAAC 1114

Qy        497 AsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGluGlyLysLysLeu 516
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Db       1115 AATGGCTACATCCTCTCTCATCCTGACCTCCGACCTTTGTACAGAGAAGGCAAGAAGCTG 1174

Qy        517 LysProLysProAsnTyrAsnSerValAspLeuSerGluValGluTrpGluAspGlnAla 536
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Qy        537 GluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeuSerMetAspValLys 556
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Db       1535 CAACTGGAAGCTGTGGTTCGTTTCCTGACAGGGGTGGATCCAGACCTGGAGTGTGAG 1591

RESULT 5
AK044427
LOCUS       AK044427               3230 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult retina cDNA, RIKEN full-length enriched library,
```

clone:A930012E17 product:hypothetical von Willebrand factor type A domain containing protein, full insert sequence.
ACCESSION AK044427
VERSION AK044427.1 GI:26090352
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3230)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
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ORIGIN

Alignment Scores:

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Percent Similarity:	43.67%	Conservative:	24
Best Local Similarity:	41.18%	Mismatches:	21
Query Match:	31.44%	Indels:	523
DB:	3	Gaps:	1

US-09-833-222A-10 (1-1090) x AK044427 (1-3230)

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Qy         91 HisGluPheAsnGluSerLeuVal---------------------------------- 98
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Db        580 CATGAGTTCAATGCATCTCTGGT-GGTAAGTCCTCTGGGGAGCGGGTGCTAGGCCGGCTG 638

Qy         98 ---------------------------------------------------------- 98

Db        639 ATTGGCTCTGCCCCACCCCCATGGCAGCTGGAGGACCAGCTGTGAGCAGATCTGAGCAGC 698

Qy         98 ---------------------------------------------------------- 98

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Qy         98 ---------------------------------------------------------- 98

Db        759 TTCCACCTCCTAAGGCTCTCGGAGAAGGAATAGAATAAACATGTGGTGTGGGGGTGGGTC 818

Qy         98 ---------------------------------------------------------- 98

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Qy         98 ---------------------------------------------------------- 98

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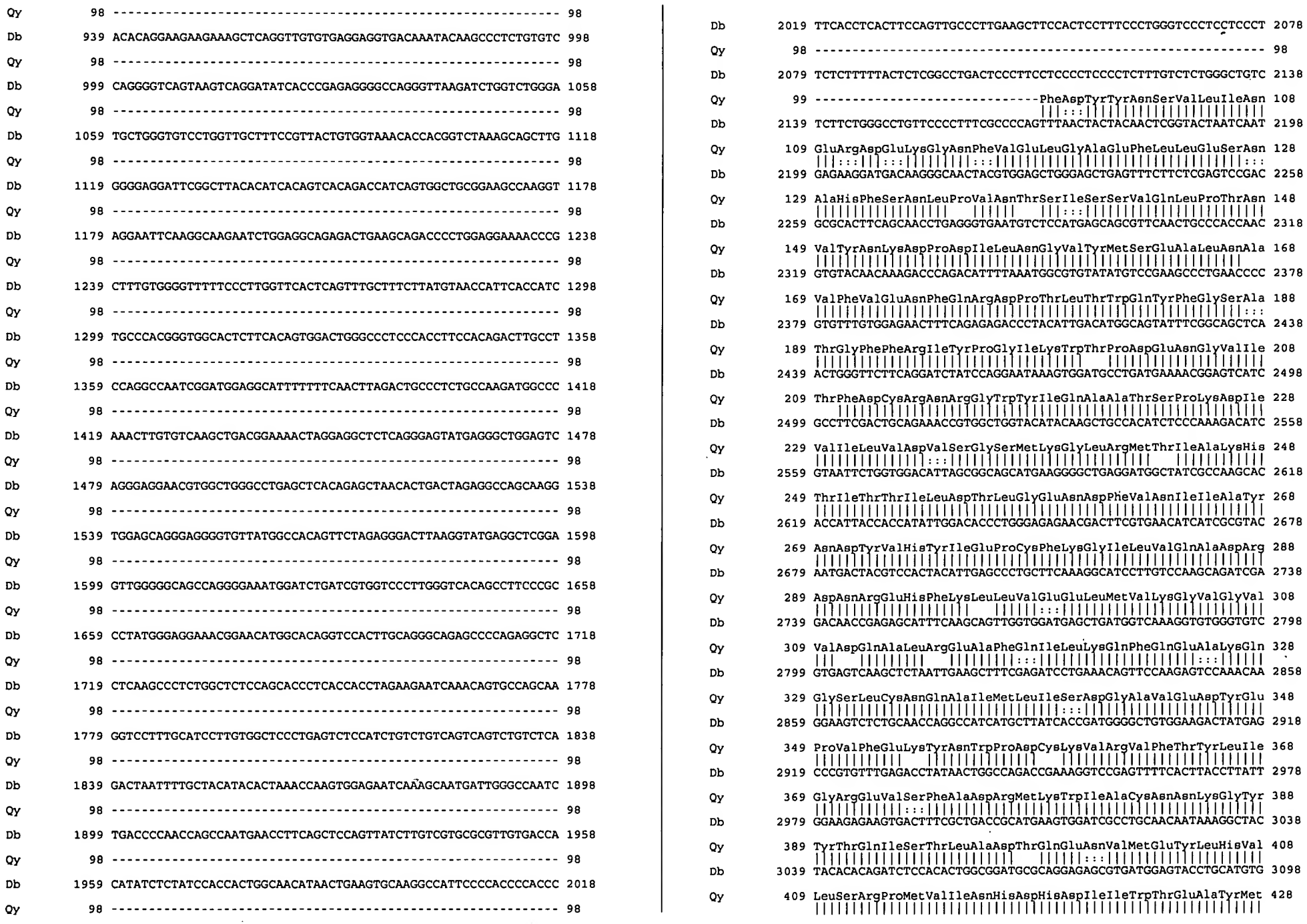
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Db 939 ACACAGGAAGAAGAAAGCTCAGGTTGTGTGAGGAGGTGACAAATACAAGCCCTCTGTGTC 998
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Qy 98 ---------- 98
Db 1119 GGGGAGGATTCGGCTTACACATCACAGTCACAGACCATCAGTGGCTGCGGAAGCCAAGGT 1178
Qy 98 ---------- 98
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Qy 98 ---------- 98
Db 1239 CTTTGTGGGGTTTTTCCCTTGGTTCACTCAGTTTGCTTTCTTATGTAACCATTCACCATC 1298
Qy 98 ---------- 98
Db 1299 TGCCCACGGGTGGCACTCTTCACAGTGGACTGGGCCCTCCCACCTTCCACAGACTTGCCT 1358
Qy 98 ---------- 98
Db 1359 CCAGGCCAATCGGATGGAGGCATTTTTTTCAACTTAGACTGCCCTCTGCCAAGATGGCCC 1418
Qy 98 ---------- 98
Db 1419 AAACTTGTGTCAAGCTGACGGAAAACTAGGAGGCTCTCAGGGAGTATGAGGGCTGGAGTC 1478
Qy 98 ---------- 98
Db 1479 AGGGAGGAACGTGGCTGGGCCTGAGCTCACAGAGCTAACACTGACTAGAGGCCAGCAAGG 1538
Qy 98 ---------- 98
Db 1539 TGGAGCAGGGAGGGGTGTTATGGCCACAGTTCTAGAGGGACTTAAGGTATGAGGCTCGGA 1598
Qy 98 ---------- 98
Db 1599 GTTGGGGGCAGCCAGGGGAAATGGATCTGATCGTGGTCCCTTGGGTCACAGCCTTCCCGC 1658
Qy 98 ---------- 98
Db 1659 CCTATGGGAGGAAACGGAACATGGCACAGGTCCACTTGCAGGGCAGAGCCCCAGAGGCTC 1718
Qy 98 ---------- 98
Db 1719 CTCAAGCCCTCTGGCTCTCCAGCACCCTCACCACCTAGAAGAATCAAACAGTGCCAGCAA 1778
Qy 98 ---------- 98
Db 1779 GGTCCTTTGCATCCTTGTGGCTCCCTGAGTCTCCATCTGTCTGTCAGTCAGTCTGTCTCA 1838
Qy 98 ---------- 98
Db 1839 GACTAATTTTGCTACATACACTAAACCAAGTGGAGAATCAAAGCAATGATTGGGCCAATC 1898
Qy 98 ---------- 98
Db 1899 TGACCCCAACCAGCCAATGAACCTTCAGCTCCAGTTATCTTGTCGTGCGCGTTGTGACCA 1958
Qy 98 ---------- 98
Db 1959 CATATCTCTATCCACCACTGGCAACATAACTGAAGTGCAAGGCCATTCCCCACCCCACCC 2018
Qy 98 ---------- 98
Db 2019 TTCACCTCACTTCCAGTTGCCCTTGAAGCTTCCACTCCTTTCCCTGGGTCCCTCCTCCCT 2078
Qy 98 ---------- 98
Db 2079 TCTCTTTTTACTCTCGGCCTGACTCCCTTCCTCCCCTCCCCTCTTTGTCTCTGGGCTGTC 2138
Qy 99 ----------PheAspTyrTyrAsnSerValLeuIleAsn 108
Db 2139 TCTTCTGGGCCTGTTCCCCTTTCGCCCCAGTTTAACTACTACAACTCGGTACTAATCAAT 2198
Qy 109 GluArgAspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsn 128
Db 2199 GAGAAGGATGACAAGGGCAACTACGTGGAGCTGGGAGCTGAGTTTCTTCTCGAGTCCGAC 2258
Qy 129 AlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsn 148
Db 2259 GCGCACTTCAGCAACCTGAGGGTGAATGTCTCCATGAGCAGCGTTCAACTGCCCACCAAC 2318
Qy 149 ValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAla 168
Db 2319 GTGTACAACAAAGACCCAGACATTTTAAATGGCGTGTATATGTCCGAAGCCCTGAACCCC 2378
Qy 169 ValPheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAla 188
Db 2379 GTGTTTGTGGAGAACTTTCAGAGAGACCCTACATTGACATGGCAGTATTTCGGCAGCTCA 2438
Qy 189 ThrGlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIle 208
Db 2439 ACTGGGTTCTTCAGGATCTATCCAGGAATAAAGTGGATGCCTGATGAAAACGGAGTCATC 2498
Qy 209 ThrPheAspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIle 228
Db 2499 GCCTTCGACTGCAGAAACCGTGGCTGGTACATACAAGCTGCCACATCTCCCAAAGACATC 2558
Qy 229 ValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHis 248
Db 2559 GTAATTCTGGTGGACATTAGCGGCAGCATGAAGGGGCTGAGGATGGCTATCGCCAAGCAC 2618
Qy 249 ThrIleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyr 268
Db 2619 ACCATTACCACCATATTGGACACCCTGGGAGAGAACGACTTCGTGAACATCATCGCGTAC 2678
Qy 269 AsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArg 288
Db 2679 AATGACTACGTCCACTACATTGAGCCCTGCTTCAAAGGCATCCTTGTCCAAGCAGATCGA 2738
Qy 289 AspAsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyVal 308
Db 2739 GACAACCGAGAGCATTTCAAGCAGTTGGTGGATGAGCTGATGGTCAAAGGTGTGGGTGTC 2798
Qy 309 ValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGln 328
Db 2799 GTGAGTCAAGCTCTAATTGAAGCTTTCGAGATCCTGAAACAGTTCCAAGAGTCCAAACAA 2858
Qy 329 GlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGlu 348
Db 2859 GGAAGTCTCTGCAACCAGGCCATCATGCTTATCACCGATGGGGCTGTGGAAGACTATGAG 2918
Qy 349 ProValPheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIle 368
Db 2919 CCCGTGTTTGAGACCTATAACTGGCCAGACCGAAAGGTCCGAGTTTTCACTTACCTTATT 2978
Qy 369 GlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyr 388
Db 2979 GGAAGAGAAGTGACTTTCGCTGACCGCATGAAGTGGATCGCCTGCAACAATAAAGGCTAC 3038
Qy 389 TyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisVal 408
Db 3039 TACACACAGATCTCCACACTGGCGGATGCGCAGGAGAGCGTGATGGAGTACCTGCATGTG 3098
Qy 409 LeuSerArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMet 428

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Db       3099 CTTAGCCGCCCCATGGTCATCAACCATGACCACGACATCATCTGGACAGAGGCTTACATG 3158

Qy        429 AspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMet 448
              ||||||:::|||   :::|||:::||||||||||||   ||||||||||||||||||||
Db       3159 GACAGCCGGCTCTTCACATCAGAGGCACAGAGCCTGATGCTCCTCACCACAGTGGCCATG 3218

Qy        449 ProValPheSer 452
              ||||||||||||
Db       3219 CCTGTCTTCAGC 3230

RESULT 6
BI518624
LOCUS       BI518624                 916 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603061574F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5210826 5',
            mRNA sequence.
ACCESSION   BI518624
VERSION     BI518624.1  GI:15343416
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 916)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11529  row: c  column: 19
            High quality sequence stop: 842.
FEATURES             Location/Qualifiers
     source          1. .916
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5210826"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              4.19e-136      Length:         916
Score:                  1356.00        Matches:        261
Percent Similarity:     88.89%         Conservative:   3
Best Local Similarity:  87.88%         Mismatches:     14
Query Match:            23.68%         Indels:         19
DB:                     4              Gaps:           1

US-09-833-222A-10 (1-1090) x BI518624 (1-916)

Qy        788 AlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGln 807
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAG 62

Qy        808 CysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPhe 827
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||

Db          63 TGCAGCACTGTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTC 122

Qy        828 ValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPhe 847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 GTCATCGACAACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTT 182

Qy        848 LeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGln 867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         183 CTGGGGGAGGTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAA 242

Qy        868 ValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAla 887
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         243 GTGACTATGTATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCC 302

Qy        888 GlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGlu 907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         303 CAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAG 362

Qy        908 LeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGlu 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         363 CTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAG 422

Qy        928 AlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCys 947
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         423 GCCAAAAGTGTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGC 482

Qy        948 AspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleVal 967
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Db         483 GACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTG 542

Qy        968 GluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeu 987
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         543 GAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTC 602

Qy        988 LeuLeuValThrAspProThrCysAspCysSerIleProProValLeuGlnGluAla 1007
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         603 CTCCTGGTGACAGACCCCACCTGTGACTGCAGCATCTTCCCACCGGTGCTGCAGGAGGCG 662

Qy       1008 ThrGluValLysTyr-AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuAr 1027
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         663 ACAGAAGTCAAATATTAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCC 722

Qy       1027 gArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGl 1047
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         723 GCGGCGACCAGACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGCGG 782

Qy       1047 yTrpAlaGlyPheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGl 1067
              |   :::     |||:::     |||
Db         783 CGCCTCGGACACCTCAGCCTCGCGCCCT------------------------------ 810

Qy       1067 uHisIleGlyMetProMetAsnThrProValProValLeuLeuGlyGly 1083
                                      ||||||||||||||||||||   |||
Db         811 ----------------------ACTCCTGTGCCTGTGTTGTTGCCTGGG 837

RESULT 7
AL558158
LOCUS       AL558158                 892 bp    mRNA    linear   EST 02-APR-2004
DEFINITION  AL558158 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
            Homo sapiens cDNA clone CS0DJ001YM12 5-PRIME, mRNA sequence.
ACCESSION   AL558158
VERSION     AL558158.3  GI:46183556
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 892)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:31279957.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
```

```
          2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen. This sequence belongs to sequence cluster
          6520.r,
          and it belongs to a clone representative of this cluster. For more
          information about this cluster and the virtual cDNA, see
          http://www.genoscope.cns.fr/cdna?s=CS0DJ001BG06QP1&c=6520.r.
FEATURES             Location/Qualifiers
     source          1. .892
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DJ001YM12"
                     /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
                     /cell_line="JURKAT"
                     /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
                     10-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Alignment Scores:
Pred. No.:              6.21e-132       Length:         892
Score:                  1317.50         Matches:        252
Percent Similarity:     92.39%          Conservative:   3
Best Local Similarity:  91.30%          Mismatches:     18
Query Match:            23.01%          Indels:         3
DB:                     1               Gaps:           2

US-09-833-222A-10 (1-1090) x AL558158 (1-892)

Qy        789 GlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCys 808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGC 62

Qy        809 SerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheVal 828
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db         63 AGCACTGTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTC 122

Qy        829 IleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeu 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ATCGACAACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTG 182

Qy        849 GlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnVal 868
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Db        183 GGGGAGGTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTG 242

Qy        869 ThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGln 888
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Db        243 ACTATGTATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACACAGTGCAGCCCAG 302

Qy        889 ProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeu 908
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCCCTG------CCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTG 356

Qy        909 ValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAla 928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 GTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCC 416

Qy        929 LysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAsp 948
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Db        417 AAAAGTGTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGAC 476

Qy        949 ThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGlu 968
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        477 ACGGAGTACCCCGTGTTCGTGTACNASCCGGCCATCCGGGAGGCCAACGGGATCGTGGAG 536

Qy        969 CysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeu 988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 TGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTC 596

Qy        989 LeuValThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThr 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 CTGGTGACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACA 656

Qy       1009 GluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArg 1028
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Db        657 GAAGTCAAATATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAKCTCCGCCGG 716

Qy       1029 ArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrp 1048
              |||   ||||||||||||||||||||||||||||||          :::   |||   |||
Db        717 CGAMCAGACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAG---GACTGCGGCGGC 773

Qy       1049 AlaGlyPheSerSerProAsnProLeuCysLeuGlyLeuCysProCys 1064
                    :::|||   :::|||       |||   |||       |||
Db        774 SCTCGGGACACCTCAGCCTCGCCGCCCCTACTCCYGCTGCCTGTGTGT 821

RESULT 8
CR603629
LOCUS       CR603629               1446 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DJ001YM12 of T cells (Jurkat cell line)
            Cot 10-normalized of Homo sapiens (human).
ACCESSION   CR603629
VERSION     CR603629.1  GI:50484436
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1446)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1446)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1446
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                     /db_xref="taxon:9606"
                     /clone="CS0DJ001YM12"
                     /tissue_type="T cells (Jurkat cell line) Cot
                     10-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

Alignment Scores:
Pred. No.:              2.42e-129       Length:         1446
Score:                  1297.00         Matches:        255
Percent Similarity:     89.66%          Conservative:   5
Best Local Similarity:  87.93%          Mismatches:     26
Query Match:            22.65%          Indels:         6
DB:                     3               Gaps:           2

US-09-833-222A-10 (1-1090) x CR603629 (1-1446)

Qy        789 GlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCys 808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db          3 GGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGC 62

Qy        809 SerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheVal 828
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db         63 AGCACTGTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTC 122

Qy        829 IleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeu 848
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ATCGACAACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTG 182

Qy        849 GlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnVal 868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GGGGAGGTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTG 242

Qy        869 ThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGln 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 ACTATGTATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAG 302

Qy        889 ProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeu 908
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CCCCTG------CCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTG 356

Qy        909 ValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAla 928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 GTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCC 416

Qy        929 LysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAsp 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 AAAAGTGTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGAC 476

Qy        949 ThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGlu 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 ACGGAGTACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAG 536

Qy        969 CysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeu 988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 TGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTC 596

Qy        989 LeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThr 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 CTGGTGACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACA 656

Qy       1009 Glu------ValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
              |||      :::   :::||||||||||||||||||||||||||||||||||||||||||
Db        657 GAATGGCTTCTGCA-CATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTC 715

Qy       1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046
              ||||||||||||||||||||||||||||||||||||        :::
Db        716 CGCCGGCGACCAGACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGC 775

Qy       1047 GlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGln 1066
              |||   :::     |||:::      ||||||  |||     |||   |||
Db        776 GGCGCCTCGGACACCTCAGCCTCGCCGCCCCTACTCCTGCT-GCCTGTGTGTGCCTGGGG 834

Qy       1067 GluHisIleGlyMetProMetAsnThrPro 1076
                          |||      ||||||
Db        835 GCTACTGCCCCAACTCCTGCGGTGACACCA 864

RESULT 9
CD743170/c
LOCUS       CD743170                747 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT1-bkc-o-08-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bkc-o-08-0-UI 3', mRNA sequence.
ACCESSION   CD743170
VERSION     CD743170.1  GI:32294020
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 183-231, >HERVR#LTR/Retroviral
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .747
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bkc-o-08-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                     moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                     vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
                     (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
                     3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                     3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                     hours; wt adenovirus + LPS 24 hours. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_TISSUE=Human Lung Alveolar Macrophage
                     TAG_LIB=UI-H-FT1
                     TAG_SEQ=GGCCATGCCG"
ORIGIN

Alignment Scores:
Pred. No.:                1.85e-126       Length:          747
Score:                    1266.00         Matches:         231
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              22.11%          Indels:          0
DB:                       6               Gaps:            0

US-09-833-222A-10 (1-1090) x CD743170 (1-747)
```

```
Qy        860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 CTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCAGGCCATGTGCAAACCC 688

Qy        880 SerSerHisHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACG 628

Qy        900 AlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGly 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 GCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGC 568

Qy        920 SerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLys 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 TCCTGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCACTCCCACAAACACAAG 508

Qy        940 LysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAla 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 AAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCC 448

Qy        960 IleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGln 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 ATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAG 388

Qy        980 GlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATC 328

Qy       1000 PheProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAsp 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TTCCCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGCCTCTGTCAAATGTGAC 268

Qy       1020 ArgMetArgSerGlnLysLeuArgArgArgProAspSerCysHisAlaPheHisProGlu 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 CGGATGCGCTCCCAGAAGCTCCGCCGGCGACCAGACTCCTGCCACGCCTTCCATCCAGAG 208

Qy       1040 ValArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeu 1059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GTGCGGGTTGAGGCGGATCGAGGGTGGGCTGGATTTTCATCCCCAAACCCTCTGTGCCTG 148

Qy       1060 GlyLeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProVal 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 GGTCTGTGCCCCTGCAGACAGGAGCATATAGGGATGCCAATGAACACACCTGTGCCTGTG 88

Qy       1080 LeuLeuGlyGlyAsnIleArgValTyrAlaLeu 1090
              |||||||||||||||||||||||||||||||
Db          87 CTTCTCGGGGGAAACATTCGCGTTTATGCCCTG 55

RESULT 10
BI908421
LOCUS       BI908421                853 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603067367F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5216273 5',
            mRNA sequence.
ACCESSION   BI908421
VERSION     BI908421.1  GI:16171373
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov

            Plate: LLAM11543  row: f  column: 18
            High quality sequence stop: 841.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5216273"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              3.08e-124       Length:         853
Score:                  1246.50         Matches:        247
Percent Similarity:     87.32%          Conservative:   1
Best Local Similarity:  86.97%          Mismatches:     13
Query Match:            21.77%          Indels:         23
DB:                     4               Gaps:           3

US-09-833-222A-10 (1-1090) x BI908421 (1-853)

Qy         787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          34 GCCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGG 93

Qy         807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
               |||                                           ||||||||||||
Db          94 CAG-------------------------------------------GATCTGGACTGC 108

Qy         827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         109 TTCGTCATCGACAACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGA 168

Qy         847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         169 TTTCTGGGGGAGGTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGC 228

Qy         867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla 886
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         229 CAAGTGACTATGTATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCA 288

Qy         887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGln 906
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         289 GCCCAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACGGCAACCAGGTGGCTGCTGCAG 348

Qy         907 GluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAla 926
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         349 GAGCTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCC 408

Qy         927 GluAla-LysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPr 946
               ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         409 GAGGCCAAAAAGTGTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCC 468

Qy         946 oCysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIl 966
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         469 CTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGAT 528

Qy         966 eValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLe 986
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         529 CGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCT 588

Qy         986 uLeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGl 1006
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 CCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGA 648

Qy       1006 uAlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGln-LysL 1026
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        649 GGCGACAGAAGTCAAATATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAAGC 708

Qy       1026 euArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspA 1046
                ||||||||||||||||||||||||||||||||||||||||      :::   |||
Db        709 TCCGCCGGCGACCAGACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAG---GACT 765

Qy       1046 rgGlyTrpAlaGlyPheSerSerProAsnProLeu--------------CysLeuGlyL 1061
                  |||   |||                        |||              ||||||||||
Db        766 GCGGCGGCGCCTGGACACCTCAGCTTCGCGCCCTATCCTGCTGCTGTGTGTGCCTGGGGC 825

Qy       1061 euCysPro 1063
                ||   |||
Db        826 TACTGCCC 833

RESULT 11
CO424223
LOCUS       CO424223                765 bp    mRNA    linear   EST 06-JUL-2004
DEFINITION  UI-M-HU0-crd-n-17-0-UI.r1 NIH_BMAP_HU0 Mus musculus cDNA clone
            IMAGE:30666472 5', mRNA sequence.
ACCESSION   CO424223
VERSION     CO424223.1  GI:49670350
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .765
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30666472"
                     /tissue_type="whole eye"
                     /dev_stage="newborn( 1, 5, 15 days )"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_HU0"
                     /note="Organ: Eye; Vector: pYX-Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site .Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AATAATTACG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH)."
ORIGIN
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Alignment Scores:
Pred. No.:              2.64e-122       Length:         765
Score:                  1228.00         Matches:        233
Percent Similarity:     95.29%          Conservative:   10
Best Local Similarity:  91.37%          Mismatches:     12
Query Match:            21.45%          Indels:         0
DB:                     7               Gaps:           0

US-09-833-222A-10 (1-1090) x CO424223 (1-765)

Qy        395 LeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgProMetVal 414
              |||||||||   ||||||:::||||||||||||||||||||||||||||||||||||||||
Db          1 CTGGCGGATGCGCAGGAGAGCGTGATGGAGTACCTGCATGTGCTTAGCCGCCCCATGGTC 60

Qy        415 IleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSer 434
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||   :::
Db         61 ATCAACCATGACCACGACATCATCTGGACAGAGGCTTACATGGACAGCCGGCTCTTCACA 120

Qy        435 SerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSerLysLys 454
              |||:::||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        121 TCAGAGGCACAGAGCCTGATGCTCCTCACCACAGTGGCCATGCCTGTCTTCAGCAAAAAG 180

Qy        455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        181 AATGAAACAAGATCCCATGGCATTCTCCTGGGTGTAGTGGGCTCTGACGTGACCCTAAGA 240

Qy        475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCTCATGAAGCTGGCACCCCGATATAAGCTTGGGGTGCATGGCTATGCCTTCTTGAAC 300

Qy        495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGluGlyLys 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACTAACAATGGCTACATCCTCTCTCATCCTGACCTCCGACCTTTGTACAGAGAAGGCAAG 360

Qy        515 LysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGluTrpGluAsp 534
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGCTGAGACCCAAACCCAACTACAACAGTGTGGACCTCTCAGAAGTGGAGTGGGAGGAC 420

Qy        535 GlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeuSerMetAsp 554
              |||||||||   ||||||||||||||||||||   |||||||||:::   |||||||||
Db        421 CAAGCTGAAATTCTGAGGACCGCCATGATCAATGGGGAAACCGGGTCTCACTCCATGGAC 480

Qy        555 ValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAspTyrPhePhe 574
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGAAGGTGCCACTGGACAAAGGGAAGCGAGTTCTATTCCTGACCAATGACTACTTCTTC 540

Qy        575 ThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGlu 594
              ||||||||||||||||||||||||||||||   ||||||:::||||||||||||||||
Db        541 ACAGACATCAGTGACACACCTTTCAGCCTGGGAGTGGTGCTCACCAGAGGTCATGGAGAA 600

Qy        595 TyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACATCCTCCTGGGGAACACATCTGTGGAAGAAGGCCTGCACGACTTGCTTCATCCGGAT 660

Qy        615 LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys 634
              |||   ||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGACCCTGGCCAGTGACTGGATCTACTGTATCACAGATATCGACCCGGACCACCGGAAA 720

Qy        635 LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAsp 649
              |||||||||||||||||:::::|||||||||||     |||
Db        721 CTCAGCCAACTGGAAGCTGTGGTTCGTTTCCTGACAGGGGTGGAT 765

RESULT 12
BQ919363
LOCUS       BQ919363                940 bp    mRNA    linear   EST 20-AUG-2002
DEFINITION  AGENCOURT_8779072 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6373010
            5', mRNA sequence.
ACCESSION   BQ919363
VERSION     BQ919363.1  GI:22334061
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1  (bases 1 to 940)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2549  row: l  column: 03
            High quality sequence stop: 524.
FEATURES             Location/Qualifiers
     source          1. .940
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6373010"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_18"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:                5.64e-120      Length:          940
Score:                    1208.00        Matches:         236
Percent Similarity:       83.62%         Conservative:    4
Best Local Similarity:    82.23%         Mismatches:      13
Query Match:              21.10%         Indels:          34
DB:                       5              Gaps:            3

US-09-833-222A-10 (1-1090) x BQ919363 (1-940)

Qy        787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
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Db         19 GCCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGG 78

Qy        807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
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Db         79 CAGTGCAGCACTGTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGC 138

Qy        827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
              ||||||||||||||||||||||||||||||||||||||||||
Db        139 TTCGTCATCGACAACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGA------------ 186

Qy        847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866

Db        186 ------------------------------------------------------------ 186

Qy        867 Gln-ValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAl 886
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Db        187 GAGAGTGACTATGTATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGC 246

Qy        886 aAlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGl 906
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Db        247 AGCCCAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCA 306

Qy        906 nGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAl 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GGAGCTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGC 366

Qy        926 aGluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPr 946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CGAGGCCAAAAGTGTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCC 426

Qy        946 oCysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIl 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGAT 486

Qy        966 eValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLe 986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCT 546

Qy        986 uLeuLeuLeuValThrAspProThrCysAspCysSerIleProProValLeuGlnGl 1006
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Db        547 CCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGA 606

Qy       1006 uAlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLe 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GGCGACAGAAGTCAAATATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCT 666

Qy       1026 uArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspAr 1046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CCGCCGGCGACCAGACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGGACTGCG 726

Qy       1046 g-GlyTrpAlaGly---------PheSerSerProAsnProLeuCysLeu---------- 1059
              | |||      |||           ::::::|||   |||      |||
Db        727 GCGGCGGCCTCGGACACCTCAGCCTCGCCGCCCCTACTCCTGGCTGGCTGGGNGGGGGCC 786

Qy       1060 -----GlyLeuCysPro 1063
                    |||   ||||||
Db        787 TGGGGGGCTACTGCCCC 803

RESULT 13
BI908463
LOCUS       BI908463                 777 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603069223F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218349 5',
            mRNA sequence.
ACCESSION   BI908463
VERSION     BI908463.1  GI:16171419
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11548  row: m  column: 06
            High quality sequence stop: 777.
FEATURES             Location/Qualifiers
     source          1. .777
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5218349"
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                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
```

1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	2.43e-117	Length:	777
Score:	1182.50	Matches:	233
Percent Similarity:	85.92%	Conservative:	5
Best Local Similarity:	84.12%	Mismatches:	12
Query Match:	20.65%	Indels:	29
DB:	4	Gaps:	2

US-09-833-222A-10 (1-1090) x BI908463 (1-777)

```
Qy        789 GlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCys 808
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGC 62

Qy        809 SerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheVal 828
              |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db         63 AGCACTGTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTC 122

Qy        829 IleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeu 848
              ||||||||||||||||||||||||||||||||||||
Db        123 ATCGACAACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGA------------------ 164

Qy        849 GlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGln-Va 868
                                                                  ::: ||
Db        165 ----------------------------------------------------GAGAGT 170

Qy        868 lThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGl 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 GACTATGTATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCA 230

Qy        888 nProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLe 908
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACGGCAACCAGGTGGCTGCTGCAGGAGCT 290

Qy        908 uValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAl 928
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Db        291 GGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGC 350

Qy        928 aLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAs 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 CAAAAGTGTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGA 410

Qy        948 pThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGl 968
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 CACGGAGTACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGA 470

Qy        968 uCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLe 988
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Db        471 GTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCT 530

Qy        988 uLeuValThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaTh 1008
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Db        531 CCTGGTGACAGAGCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGAC 590

Qy       1008 rGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgAr 1028
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAAGTCAAATATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCG 650

Qy       1028 gArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTr 1048
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Db        651 GCGACCAGACTCCTGGCACGCCTTCCATCCAGAGGA-CGAATGCC-CAGGACTGCGGCGG 708

Qy       1048 pAlaGlyPheSerSerProAsnPro------LeuCysLeuGlyLeuCys 1062
                |||      ||||||   :::|||      |||  |||   :::|||
Db        709 CGCCTCGGACAGCTCAGCCTCGCCGCCCCTACTCTTGCTGCCTGTGTGT 757
```

RESULT 14

AK044603

```
LOCUS       AK044603               3527 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult retina cDNA, RIKEN full-length enriched library,
            clone:A930026F23 product:calcium channel, voltage-dependent, alpha
            2/delta subunit 2, full insert sequence.
ACCESSION   AK044603
VERSION     AK044603.1  GI:26336630
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3527)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
```

```
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
          Retina RNA was provided by Dr. Stefano Gustincich (Department of
          Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA
          02115, USA) whose assistance is gratefully acknowledged. Please
          visit our web site for further details.
          URL:http://genome.gsc.riken.jp/
          URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .3527
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                     /db_xref="taxon:10090"
                     /clone="A930026F23"
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                     /dev_stage="adult"
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                     ANCNKMIMMFTDGGEDRVQDVFEKYNWPNRTVRVFTFSVGQHNYDVTPLQWMACTNKG
                     YYFEIPSIGAIRINTQEYLDVLGRPMVLAGKDAKQVQWTNVYEDALGLGLVVTGTLPV
                     FNLTQDGPGEKKNQLILGVMGIDVALNDIKRLTPNYTLGANGYVFAIDLNGYVLLHPN
                     LKPQTTNFREPVTLDFLDAELEDENKEEIRRSMIDGDKGHKQIRTLVKSLDERYIDEV
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ORIGIN

Alignment Scores:
Pred. No.:                6.04e-116      Length:          3527
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Percent Similarity:       47.77%         Conservative:    202
Best Local Similarity:    30.13%         Mismatches:      426
Query Match:              20.61%         Indels:          172
DB:                       3              Gaps:            44

US-09-833-222A-10 (1-1090) x AK044603 (1-3527)

Qy          16 TrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeu 35
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Db         231 TGGGCCCGGCGCCTGGAGCAGGAGATTGACGGTGTGATGCGGATTTTTGGAGGCGTGCAG 290

Qy          36 LeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55
                  |||::::::   |||||||||      :::      ::::::::::|||   :::
Db         291 CAGCTCCGAGAGATCTACAAGGACAATCGGAACCTGTTTGAAGTGCAGGAGAATGAACCA 350

Qy          56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75
                  :::|||||||   |||   :::   |||:::|||:::::::|||   ||||||||||:::
Db         351 CAGAAATTGGTGGAGAAAGTGGCAGGGGACATCGAGAGCCTGCTGGACAGGAAGGTCCAG 410

Qy          76 AlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
               |||::::::   |||   :::||||||||                |||   :::   :::
Db         411 GCCCTGAAGAGACTGGCTGACGCTGCAGAGAATTTCCAGAAAGCCCATCGCTGGCAGGAC 470

Qy          96 SerLeuValPheAsp---------TyrTyrAsnSerValLeuIleAsnGluArgAsp--- 111
               ::::::      :::       |||||::::::             |||   |||
Db         471 AACATCAAGGAGGAAGACATCATGTACTACGATGCCAAGGCTGACGCCGAGCTGGATGAC 530

Qy         112 ------------------GluLysGlyAsnPheValGlu---LeuGlyAlaGluPheLeu 124
                              |||:::|||:::           |||     :::|||:::
Db         531 CCTGAGAGTGAAGATATGGAGAGGGGATCCAAGACCAGCGCCTTAAGGCTGGACTTCATC 590

Qy         125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
                  :::   |||      |||   |||      ||||||   |||   ::::::||||||
Db         591 GAGGACCCAAAC------TTCAAGAAC---AAAGTCAACTATTCATACACGGCTGTGCAG 641

Qy         145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
               :::||||||:::::|||                |||||||||   :::     :::|||
Db         642 ATCCCCACAGACATCTACAAAGGCTCTACCGTCATCCTCAATGAGCTTAACTGGACAGAG 701

Qy         165 AlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyr 184
               ||||||      ||||||:::||||||   ::::::||||||||||||   ||||||
Db         702 GCCCTGGAGAACGTCTTCATTGAGAACCGTAGGCAAGACCCTACACTGTTGTGGCAAGTC 761

Qy         185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGlu 204
               ||||||||||||||||||      |||   ||||||          |||         :::
Db         762 TTTGGCAGTGCCACGGGAGTCACTCGCTATTACCCAGCCACACCATGGCGAGCCCCCAAG 821

Qy         205 AsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSer 224
                  :::      :::|||   |||   |||   ||||||||||||   |||:::|||
Db         822 AAG---ATTGACCTGTACGATGTCAGAAGACGACCCTGGTATATACAGGGGGCCTCATCA 878

Qy         225 ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr 244
               |||||||||:::||||||:::||||||||||||||||||:::   ||||||   :::
Db         879 CCCAAGGACATGGTCATCATTGTGGATGTGAGTGGGAGCGTGAGCGGCCTGACTCTGAAG 938

Qy         245 IleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsn 264
               :::   |||   ::::::      :::||||||||||||   ::::::|||:::||||||
Db         939 CTGATGAAGACGTCCGTCTGTGAGATGCTAGACACGCTCTCTGATGATGACTATGTGAAC 998

Qy         265 IleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
               :::   ::::::|||:::          :::      ||||||          ||||||
Db         999 GTGGCCTCATTCAACGAGAAGGCGCAGCCTGTGTCT---TGCTTCACACAC---CTGGTG 1052

Qy         285 GlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLys 304
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Db        1053 CAGGCCAATGTGCGTAACAAGAAGGTGTTCAAGGAAGCTGTGCAGGGCATGGTGGCCAAG 1112

Qy         305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
               |||                        ||||||      |||:::
Db        1113 GGCACCACAGGCTACAAGGCCGGCTTTGAGTATGCCTTTGACCAGCTACAGAATTCCAAC 1172

Qy         325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
                  :::                |||||:::   ||||||:::   :::|||||||
Db        1173 ATCACGCGGGCTAAC------TGCAATAAGATGATCATGATGTTCACGGATGGGGGTGAG 1226

Qy         345 GluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLysValArgValPhe 364
               :::      :::   |||||||||||||||||||||:::      ||||||||||||
Db        1227 GATCGCGTGCAGGATGTCTTCGAAAAGTACAATTGGCCCAATCGGACGGTACGTGTGTTC 1286

Qy         365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn 384
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Qy         385 AsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
               ||||||||||||||   :::|||   ::::::      :::   |||      |||
Db        1347 AACAAAGGTTACTATTTTGAGATCCCTTCCATCGGAGCCATCCGCATCAACACACAGGAA 1406

Qy         405 TyrLeuHisValLeuSerArgProMetValIle------AsnHisAspHisAspIleIle 422
               ||||||   ||||||   ||||||||||:::           :::
Db        1407 TACCTGGATGTGCTGGGTAGGCCCATGGTACTGGCAGGCAAGGACGCCAAGCAAGTGCAA 1466
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Qy 423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
Db 1467 TGGACAAACGTGTATGAAGAT--------------------GCACTGGGGCTGGGGTTG 1505
Qy 443 LeuThrThrValAlaMetProValPheSer-----------------------LysLys 454
Db 1506 GTGGTAACAGGAACTCTCCCTGTTTTCAACCTGACACAGGATGGCCCTGGGGAAAAGAAG 1565
Qy 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
Db 1566 AACCAG--------------TTAATCCTGGGTGTCATGGGCATCGATGTGGCCTTGAAT 1610
Qy 475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
Db 1611 GACATCAAAAGGCTGACTCCCAACTACACACTCGGCGCCAATGGCTATGTGTTCGCCATC 1670
Qy 495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu---------TyrArg 511
Db 1671 GACCTGAACGGCTACGTGTTGCTACATCCCAATCTCAAGCCCCAGACTACCAACTTCCGG 1730
Qy 512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
Db 1731 GAGCCTGTGACCTTG-------------------------GACTTCCTGGACGCAGAG 1763
Qy 532 TrpGluAspGln---AlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db 1764 CTGGAAGATGAGAACAAGGAGGAGATCCGTCGCAGCATGATTGACGGCGACAAAGGCCAC 1823
Qy 551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
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Qy 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db 1884 AACTACACCTGGGTGCCTATAAGGAGTACCAACTACAGCCTGGGGCTGGTGCTCCCA--- 1940
Qy 591 GlyHisGlyGluTyrIleLeuLeuGlyAsn------------------------------ 600
Db 1941 CCCTACAGCACCTACTACCTCCAAGCCAACCTCAGCGACCAGATCCTGCAGGTCAAGTAT 2000
Qy 601 ------------------ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp 614
Db 2001 TTTGAGTTCCTGCTTCCCAGCAGCTTTGAGTCTGAAGGACACGTTTTCATTGCTCCGAGA 2060
Qy 615 LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys 634
Db 2061 --------------------GAGTATTGC---AAGGACTTGAACGCCTCGGACAACAAC 2096
Qy 635 LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp---LeuGlu 653
Db 2097 ACCGAGTTCCTGAAGAACTTCATCGAGCTCATGGAGAAAGTGACTCCGGACTCCAAGCAG 2156
Qy 654 CysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet--- 672
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Qy 673 GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp 692
Db 2217 GAACGTGTGTGGCGGGACCAAGATCTCAAC--------------ACGTACAGCCTGCTA 2261
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Db 2262 GCCGTATTTGCTGCCACTGATGGTGGCATCACACGT----------------------- 2297
Qy 713 LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp 732
Db 2298 --------------------GTCTTCCCGAACAAGGCAGCCGAAGACTGGACAGAAAAC 2336
Qy 733 ArgPheProLeu---------TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
Db 2337 CCTGAACCCTTCAATGCCAGCTTCTACCGTCGCAGCCTGGATAAC------CATGGTTAT 2390
Qy 750 ValPheAsn--------------------LeuArgTrpAlaGluGlyPro---GluSer 761
Db 2391 ATCTTCAAGCCCCCACACCAGGACTCCCTGTTAAGA-----------CCACTGGAGCTG 2438
Qy 762 AlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLysArg 781
Db 2439 GAGAATGACACAGTAGGTGTCCTCGTCAGCACAGCTGTGGAGCTCAGTCTAGGTCGTCGC 2498
Qy 782 ThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPhe 801
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Qy 802 TrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGln----------- 817
Db 2559 AAGGTGCTGGCCAGCAACCGTACCCATCAGGACCAACCTCAGAAGCAGTGCGGCCCCAGC 2618
Qy 818 ---------------SerCysGlu------AspSerAspLeuAspCysPheValIleAsp 830
Db 2619 AGCCACTGTGAGATGGACTGCGAGGTTAACAACGAGGATCTACTCTGTGTCCTCATTGAT 2678
Qy 831 AsnAsnGlyPheIleLeuIleSerLysArgSerArg---------GluThrGlyArgPhe 847
Db 2679 GACGGAGGGTTCCTGGTGCTGTCAAACCAGAACCATCAGTGGGACCAGGTTGGCAGATTC 2738
Qy 848 LeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGln 867
Db 2739 TTCAGTGAGGTGGATGCCAACCTGATGCTGGCACTGTACAATAACTCCTTCTACACCCGA 2798
Qy 868 ValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAla 887
Db 2799 AAGGAATCCTATGACTATCAGGCAGCCTGTGCCCCTCAGCCTCCTGGGAACCTGGGTGCT 2858
Qy 888 GlnPro---------LeuValSerProIleSerAlaPheLeu------------------ 898
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Qy 899 ThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrp 918
Db 2919 TCTGCTGCCGCCTGGTCCTTATTCCAGCAGCTACTCTATGGTCTC---------ATCTAT 2969
Qy 919 GlySerTrpTyrAspArgGly---------AlaGluAlaLysSerValPheHisHisSer 935
Db 2970 CACAGCTGGTTCCAGGCAGACCCGGCAGAAGCTGAGGGCAGCCCCGAGACGCGCGAGAGC 3029
Qy 936 HisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPheVal 955
Db 3030 AGCTGCGTCATGAAACAG--------------------ACCCAGTAC------------ 3056
Qy 956 TyrGlnProAlaIleArgGluAla---AsnGlyIleValGluCysGlyProCysGlnLys 974
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Qy 975 ValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAsp---Pro 993
Db 3117 CTGTTCCATGCGCAGAGACTGACCAACACCAATCTCCTGTTCGTGGTGGCCGAGAAGCCG 3176
Qy 994 ThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluValLysTyrAsn 1013
Db 3177 CTGTGCAGCCAGTGCGAGGCGGGCCGGCTGCTGCAGAAG------GAGACACACTCGGAC 3230
Qy 1014 AlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgProAspSerCys 1033
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Qy 1034 HisAlaPheHis---ProGluValArgValGluAlaAspArgGlyTrpAlaGlyPhe--- 1051
Db 3291 TTTGACTACAATGCGACGGAAGATACCTCAGACTGTGGCCGCGGA---GCCTCCTTCCCT 3347
Qy 1052 ---------------------SerSerProAsnProLeuCysLeuGlyLeuCysProCys 1064
Db 3348 CCGTCGCTGGGCGTCTTGGTTTCCTTGCAGCTTTGCTCCTCCTGGGCCTGCCACCTCGG 3407
Qy 1065 ArgGlnGluHisIle 1069
Db

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Db       3408 CCGCAGCCTCAAGTC 3422

RESULT 15
BG436760
LOCUS       BG436760                725 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602489181F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4620980 5',
            mRNA sequence.
ACCESSION   BG436760
VERSION     BG436760.1  GI:13343177
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1383  row: b  column: 21
            High quality sequence stop: 723.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4620980"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_18"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.14e-114      Length:         725
Score:                  1157.50        Matches:        225
Percent Similarity:     88.98%         Conservative:   1
Best Local Similarity:  88.58%         Mismatches:     3
Query Match:            20.21%         Indels:         27
DB:                     4              Gaps:           1

US-09-833-222A-10 (1-1090) x BG436760 (1-725)

Qy        787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
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Db         38 GCCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGG 97

Qy        807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db         98 CAGTGCAGCACTGTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGC 157

Qy        827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 TTCGTCATCGACAACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGA---------- 205

Qy        847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866

Db        205 ------------------------------------------------------------ 205

Qy        867 Gln-ValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAl 886
                  ::: |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GAGAGTGACTATGTATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGC 265

Qy        886 aAlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGl 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 AGCCCAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCA 325

Qy        906 nGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAl 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 GGAGCTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGC 385

Qy        926 aGluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPr 946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 CGAGGCCAAAAGTGTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCC 445

Qy        946 oCysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIl 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 CTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGAT 505

Qy        966 eValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLe 986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 CGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCT 565

Qy        986 uLeuLeuLeuValThrAspProThrCysAspCysSerIleProProValLeuGlnGl 1006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 CCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGA 625

Qy       1006 uAlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLe 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 GGCGACAGAAGTCAAATATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCT 685

Qy       1026 uArgArgArgProAspSerCysHisAlaPheHisProGlu 1039
              |  ||||||  ||||||||||||||||||||||||||||
Db        686 CCG-CGGCGACA-GACTCCTGCCACGCCTTCCATCCAGAG 723

Search completed: November 17, 2005, 05:33:34
Job time : 8110 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 16, 2005, 03:13:48 ; Search time 49 Seconds
(without alignments)
2140.332 Million cell updates/sec

Title: US-09-833-222A-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTPVPVLLGGNIRVYAL 1090

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3422	59.8	1091	2	T30256	calcium channel al
2	1089	19.0	1106	1	CHRBA2	calcium channel pr
3	1077.5	18.8	1091	2	JH0565	calcium channel al
4	1056.5	18.5	1091	2	A44147	calcium channel pr
5	638.5	11.2	734	2	S44617	C50C3.11 protein -
6	543	9.5	1148	2	T18770	probable calcium c
7	209.5	3.7	1450	2	C86880	hypothetical prote
8	175	3.1	946	1	IYHU2	inter-alpha-trypsi
9	172.5	3.0	946	2	JC5575	inter-alpha-trypsi
10	166.5	2.9	946	2	S54354	inter-alpha-inhibi
11	164.5	2.9	930	2	JX0368	inter-alpha-trypsi
12	150.5	2.6	889	2	JC5576	inter-alpha-trypsi
13	148.5	2.6	886	2	S54355	inter-alpha-trypsi
14	146.5	2.6	885	2	S30350	inter-alpha-trypsi
15	145.5	2.5	2819	2	A90551	conserved hypothet
16	144.5	2.5	921	2	JC4625	inter-alpha-trypsi
17	144	2.5	820	2	AD2357	hypothetical prote
18	144	2.5	1091	2	C95133	exonuclease RexB [
19	144	2.5	1091	2	G98001	second chain of ma
20	143	2.5	655	2	S59836	hypothetical prote
21	142	2.5	911	2	A39967	inter-alpha-trypsi
22	140.5	2.5	570	2	AC2356	hypothetical prote
23	135.5	2.4	676	2	T47637	hypothetical prote
24	135	2.4	436	2	E90261	hypothetical prote
25	134.5	2.3	1276	2	S11455	botulinum neurotox
26	134.5	2.3	1329	2	AE1901	WD-repeat containi
27	134	2.3	1073	2	S14032	kinesin-related pr
28	132.5	2.3	918	2	E90542	lipoprotein [impor
29	131.5	2.3	2280	2	T38906	acetyl-CoA carboxy
30	131	2.3	1085	2	T38378	kinesin-like prote
31	129.5	2.3	587	2	I64023	hypothetical prote
32	129.5	2.3	906	2	D82899	alanyl-tRNA synthe
33	129.5	2.3	1188	2	F64367	pyruvate, water di
34	129	2.3	802	2	C90326	hypothetical prote
35	129	2.3	932	2	JC5953	inter-alpha-inhibi
36	129	2.3	8243	2	T31307	type I fatty acid
37	128	2.2	689	2	F84811	probable retroelem
38	128	2.2	914	2	JC5574	inter-alpha-trypsi
39	127.5	2.2	709	2	AD2843	methyl-accepting c
40	127.5	2.2	717	2	E97620	methyl-accepting c
41	127	2.2	629	2	C83107	chemotactic transd
42	126.5	2.2	1411	2	S55123	hypothetical prote
43	125.5	2.2	2279	2	T42531	acetyl-CoA carboxy
44	124.5	2.2	885	2	AB1944	ferrichrome iron r
45	123.5	2.2	2670	2	T37919	GCN1 homolog - fis

ALIGNMENTS

RESULT 1
T30256
calcium channel alpha-2-delta-C chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30256
R;Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A;Title: Molecular diversity of the calcium channel alpha2delta subunit.
A;Reference number: Z20794
A;Accession: T30256
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1091 <KLU>
A;Cross-references: UNIPROT:Q9Z1L5; EMBL:AJ010949; PIDN:CAA09423.1
A;Experimental source: brain
C;Superfamily: calcium channel alpha-2 chain

Query Match 59.8%; Score 3422; DB 2; Length 1091;
Best Local Similarity 60.0%; Pred. No. 1.5e-217;
Matches 627; Conservative 188; Mismatches 212; Indels 18; Gaps 6;

```
Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
              |||||  |||:: :   ||||| |||||||: |  : |||:|||:||:| :: || |  :
Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKIMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
              | |||: |||||||| | |||:  | ::|:|:|||||||: |||:||| ||:|  | ||:
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
              ||||| |:| ||:|||:|||||  |:|||| ||:|| |||:|| |||:| |||||||  |||
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
              | |||||| ||||||| |||||| ||||||||||:|||||||||||||:|||| |:::
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
              ||||||::|| ||| ||: :||:|||  | |||||| |:|||:  :::|  ||:|::| |
Db        282 ILDTLGDDDFFNIITYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
              | ||| ||  |    |||:|:||||||:|||| |: :| |||||| |||:||||||||
Db        342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
              :||| :||:|| |||::|||||||| ||||||||||||||| ||: :||::|||||:|| |
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQA----QSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVH 488
                :|     | | |:||||||||||:||||| ||||||||:|| ::||:|  |:||||:|
```

```
Db        462 PQAQKLADDQGLVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLGIH 521

Qy        489 GYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRET 548
              ||||  |||||||:||:||||| |||| : ||||:||||||||||: : || ||:||:|
Db        522 GYAFAITNNGYILTHPELRPLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNRKT 580

Qy        549 GTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLH 608
              |  ||:||  :||||||| :||||::||| ||||||  ||||||:|   || ::|||||
Db        581 GKFSMEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEGLH 640

Qy        609 DLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVV 668
              || |||::|| :| || ||: |:|| ||||||:  :|  |:| |:||:||::||||||||
Db        641 DLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVV 700

Qy        669 TAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASV 728
              :||:|||||:|||| || |:  |::|||||| || | :||||:|:::::: ||   |: ::
Db        701 SAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENI 760

Qy        729 FTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAA 788
              |  | |||||||:|:|  |||||::: :: |  :  :  ||||||:: :  :::: : ||
Db        761 FNADHFPLWYRRAAEQIAGSFVYSIPFSTG--TVNKSNVVTASTSIQLLDERKSPVVAAV 818

Qy        789 GVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFL 848
              |:|||||| |||||  |:|||:::||  : ||:|  ::|::|||||||:|:   :|| |
Db        819 GIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFF 878

Qy        849 GEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQEL 908
              |||:|||: :||:|| | ::|:|||||||: :     :|  |: |  |||:| :|:: ||
Db        879 GEVEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDSAHGLLDPYKAFLSAAKWIMTEL 938

Qy        909 VLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVE 968
              ||||:|:::  ||:     ||:        | :  |:||||||| || :  |:|  | :
Db        939 VLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIA 990

Qy        969 CGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRR 1028
              |  | | ||:||||:||| ::| | :|  |     |:     |::|| |:||:|:::||:||
Db        991 CEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKIRR 1050

Qy       1029 RPDSCHAFHPEVRVEADRGWAGFSS 1053
              ||:||| ||||   |  |   | ||
Db       1051 RPESCHGFHPE---ENARECGGASS 1072
```

RESULT 2
CHRBA2
calcium channel protein alpha-2 chain precursor - rabbit
N;Alternate names: dihydropyridine-binding protein, 140K
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: S10579; A39518; A33409
R;Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbe
Science 241, 1661-1664, 1988
A;Title: Sequence and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of
A;Reference number: S10579; MUID:88336904; PMID:2458626
A;Accession: S10579
A;Molecule type: mRNA
A;Residues: 1-1106 <ELL>
A;Cross-references: UNIPROT:P13806; EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g1647
A;Note: 57-Asn, 106-Lys, and deletion of 620-Ser were also found
R;Jay, S.D.; Sharp, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.
J. Biol. Chem. 266, 3287-3293, 1991
A;Title: Structural characterization of the dihydropyridine-sensitive calcium channel al
A;Reference number: A39518; MUID:91131638; PMID:1847144
A;Accession: A39518
A;Molecule type: protein
A;Residues: 961-973 <JAY>
A;Note: this sequence represents the amino end of a glycosylated peptide that appears af
e at the amino end and identical molecular weights (17K) following deglycosylation
R;Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R.
Biochemistry 28, 7820-7828, 1989
A;Title: Subunit composition of the purified dihydropyridine binding protein from skelet
A;Reference number: A33409; MUID:90122765; PMID:2558713
A;Accession: A33409
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-44,'S',46-47 <HAM>
C;Superfamily: calcium channel alpha-2 chain
C;Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phospho
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-1106/Product: calcium channel alpha-2 chain #status predicted <MAT>
F;94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:

  Query Match   19.0%; Score 1089; DB 1; Length 1106;
  Best Local Similarity 28.0%; Pred. No. 2e-63;
  Matches 315; Conservative 222; Mismatches 431; Indels 156; Gaps   44;

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Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
              :| | |    ||        ||   |  |: :  :|  :  :||   : |:| :|
Db         35 IKSWVDKMQEDLVTLAKTASGVHQLVDIYEKYQDLYTVEPNNARQLVEIAARDIEKLLSN 94

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFD---YYNSVLINERDEKGNFVELGAE-----FL 124
              : :|:  |   ||:    |:: |    :  |||:   :: | : |  | |::     |:
Db         95 RSKALVRLALEAEKVQAAHQWREDFASNEVVYYNAK--DDLDPEKNDSEPGSQRIKPVFI 152

Qy        125 LESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQY 184
              ::|       |:   ::| :||::|     :|| :  : ||: || :| : ||:| ||
Db        153 DDAN---FRRQVSYQHAAVHIPTDIYEGSTIVLNELNWTSALDDVFKKNREEDPSLLWQV 209

Qy        185 FGSATGFFRIYPGIKWTPDE---NGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGL 241
              |||||  | ||   | :    | :  :| | | |||| | ||||::|||||||: ||
Db        210 FGSATGLARYYPASPWVDNSRTPNKIDLYDVRRRPWYIQGAASPKDMLILVDVSGSVSGL 269

Qy        242 RMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEEL 301
              : : : ::: :|:|| ::|||: ::|    :  ||:  ||||:  |::  |  |  :
Db        270 TLKLIRTSVSEMLETLSDDDFVNVASFNSNAQDVS-CFQH-LVQANVRNKKVLKDAVNNI 327

Qy        302 MVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKV 361
              ||:    :    ||: |  :  ::    ||: ||| :||  |  : :| |||  | ||
Db        328 TAKGITDYKKGFSFAFEQLLNYNVSRAN--CNKIIMLFTDGGEERAQEIFAKYN-KDKKV 384

Qy        362 RVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHD--H 419
              ||||: :|:       ::|:|| ||||| :| ::   : |  ||| || ||||:  |
Db        385 RVFTFSVGQHNYDRGPIQWMACENKGYYYEIPSIGAIRINTQEYLDVLGRPMVLAGDKAK 444

Qy        420 DIIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFS----KKNETR-SHGILLGVVGSDVALR 474
              : ||  |:|       |  | |: |  :|||:     :|:|   : ::|||:| ||:|
Db        445 QVQWTNVYLD-------ALELGLVITGTLPVFNITGQFENKTNLKNQLILGVMGVDVSLE 497

Qy        475 ELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKL----------KPKPNYN- 523
              :: :| ||: |  :|| |    |||:| ||:|:|     | :          | :||
Db        498 DIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQP-----KPIGVGIPTINLRKRRPNVQN 552

Qy        524 -------SVDLSEVEWEDQAE-SLRTAMINRETGTLSMDVKVP------MDKGKRVLFLT 569
                    ::|  : | |:  :  :|  ||: |:|  :     |        :||| |
Db        553 PKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRT---- 608

Qy        570 NDYFFTDISDTPFSLGAVLSRGHGEYIL---LGNTSVEEGLHDLLHPD------LALAGD 620
                | :| :: | :|  |::   :  | :   :  |  :    : | ||
Db        609 --YTWTPVNGTDYSSLALVLPTYSFYYIKAKIEETITQARYSETLKPDNFEESGYTFLAP 666

Qy        621 WIYCITDIDPDHRKLSQLEAMIRFLTRKDP-DLECDEELVREVLFDAVVTAPM-EAYWTA 678
              || :|: |       |      |: || | :  |: :|:  || ||  |  : : ||:
Db        667 RDYC-SDLKPSDNNTEFLLNFNEFIDRKTPNNPSCNTDLINRVLLDAGFTNELVQNYWS- 724

Qy        679 LALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWY 738
                  :::   |   |: |  |: |     |  ::  :      ||      |        |
Db        725 -----KQKNIKGVKARFVVTDGGITR----VYPKEAGENWQENPETYEDSF--------Y 767

Qy        739 RQASEHPAGSFVFNLRW--AEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEF 796
              ::: ::   ::||  :   || :   ::|  | || : :  :    |  |::: :
Db        768 KRSLDN--DNYVFTAPYFNKSGPGAYESGIMV--SKAVEIYIQGKLLKPAVVGIKIDVNS 823

Qy        797 LQRKFWAATRQ--CSTVDGPYTQSCEDSD-LDCFVIDNNGFILISKR---SRETGRFLGE 850
                |   : :  |:   ||      :|| :|| ::|: ||:|::     : : ||| ||
Db        824 WIENFTKTSIRDPCA---GPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGE 880
```

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Qy     851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKP------SSHHSAAQPLVS---PISAFLTAT 901
Db     881 IDPSLMRHLVNISVYAFNKSYDYQSVCEPGAAPKQGAGHRSAYVPSIADILQIGWWATAA 940

Qy     902 RW-LLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPL------QPCDTEYPVF 954
Db     941 AWSILQQFLLSLT--------FPRLLEAADM--------EDDDFTASMSKQSCITEQTQY 984

Qy     955 VYQPAIREANGIVECGPCQKVFVVQQIPNSNLLLLVTDP--TCDCSIFPPVLQEATEVKY 1012
Db     985 FFDNDSKSFSGVLDCGNCSRIFHVEKLMNTNLIFIMVESKGTCPCDTRLLIQAEQTS--- 1041

Qy    1013 NASVKCDRMRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNP 1056
Db    1042 DGPDPCDMVKQPRYRKGPDVC--FDNNV-LEDYTDCGGVSGLNP 1082
```

RESULT 3
JH0565
calcium channel alpha-2b chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JH0565
R;Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B.;
Neuron 8, 71-84, 1992
A;Title: Structure and functional expression of alpha1, alpha2, and beta subunits of a r
A;Reference number: JH0564; MUID:92110010; PMID:1309651
A;Accession: JH0565
A;Molecule type: mRNA
A;Residues: 1-1091 <WIL>
A;Cross-references: UNIPROT:P54289; GB:M76559; NID:g179761; PIDN:AAA51903.1; PID:g179762
A;Experimental source: basal ganglia
A;Note: several conflicts are found between GenBank submission, authors' translation in
C;Comment: This protein is a subunit of the voltage dependent calcium channel.
C;Superfamily: calcium channel alpha-2 chain
C;Keywords: glycoprotein; phosphoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>
F;32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase C)
F;91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta
F;92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: carbo
F;501/Binding site: phosphate (Thr) (covalent) #status predicted
F;833/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic

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  Query Match            18.8%;  Score 1077.5;  DB 2;  Length 1091;
  Best Local Similarity  28.3%;  Pred. No. 1.1e-62;
  Matches  315;  Conservative  217;  Mismatches  432;  Indels  151;  Gaps   44;

Qy      13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
Db      33 IKSWVDKMQEDLVTLAKTASGVNQLVDIYEKYQDLYTVEPNNARQLVEIAARDIEKLLSN 92

Qy      73 KVEAVQNLVEAAEEADLNHEFNESLVFD---YYNSVLINERDEKGNFVELGAE-----FL 124
Db      93 RSKALVSLALEAEKVQAAHQWREDFASNEVVYYNAK--DDLDPEKNDSEPGSQRIKPVFI 150

Qy     125 LESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQY 184
Db     151 EDAN---FGRQISYQHAAVHIPTDIYEGSTIVLNELNWTSALDEVFKKNREEDPSLLWQV 207

Qy     185 FGSATGFFRIYPGIKWTPDE---NGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGL 241
Db     208 FGSATGLARYYPASPWVDNSRTPNKIDLYDVRRRPWYIQGAASPKDMLILVDVSGSVSGL 267

Qy     242 RMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEEL 301
Db     268 TLKLIRTSVSEMLETLSDDDFVNVASFNSNAQDVS-CFQH-LVQANVRNKKVLKDAVNNI 325

Qy     302 MVKGVGVVDQALREAPQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKV 361
Db     326 TAKGITDYKKGFSFAFEQLLNYNVSRAN--CNKIIMLFTDGGEERAQEIFNKYN-KDKKV 382

Qy     362 RVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHD--H 419
Db     383 RVFRFSVGQHNYERGPIQWMACENKGYYYEIPSIGAIRINTQEYLDVLGRPMVLAGDKAK 442

Qy     420 DIIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFS----KKNETR-SHGILLGVVGSDVALR 474
Db     443 QVQWTNVYLD-------ALELGLVITGTLPVFNITGQFENKTNLKNQLILGVMGVDVSLE 495

Qy     475 ELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWED 534
Db     496 DIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQP--KNPKSQEPV----TLDFLDAELEN 549

Qy     535 QAE-SLRTAMINRETGTLSMDVKVP------MDKGKRVLFLTNDYFFTDISDTPFSLGAV 587
Db     550 DIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRT------YTWTPVNGTDYSLALV 603

Qy     588 LSRGHGEYILLGNTSVEEGL------------HDLLHPD------LALAGDWIYCITDID 629
Db     604 LPTYSFYYI---KAKLEETITQARSKKGKMKDSETLKPDNFEESGYTFIAPRDYC-NDLK 659

Qy     630 PDHRKLSQLEAMIRFLTRKDP-DLECDEELVREVLFDAVVTAPM-EAYWTALALNMSEES 687
Db     660 ISDNNTEFLLNFNEFIDRKTPNNPSCNADLINRVLLDAGFTNELVQNYWS------KQKN 713

Qy     688 EHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAG 747
Db     714 IKGVKARFVVTDGGITR----VYPKEAGENWQENPETYEDSF--------YKRSLDN--D 759

Qy     748 SFVFNLRW--AEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAAT 805
Db     760 NYVFTAPYFNKSGPGAYESGIMV--SKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTS 817

Qy     806 RQ--CSTVDGPYTQSCEDSD-LDCFVIDNNGFILISKR---SRETGRFLGEVDGAVLTQL 859
Db     818 IRDPCA---GPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHL 874

Qy     860 LSMGVFSQVTMYDYQAMCKP------SSHHSAAQPLVS---PISAFLTATRW-LLQELV 909
Db     875 VNISVYAFNKSYDYQSVCEPGAAPKQGAGHRSAYVPSVADILQIGWWATAAAWSILQQFL 934

Qy     910 LFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPL------QPCDTEYPVFVYQPAIREA 963
Db     935 LSLT--------FPRLLEAVEM--------EDDDFTASLSKQSCITEQTQYFFDNDSKSF 978

Qy     964 NGIVECGPCQKVFVVQQIPNSNLLLLVTDP--TCDCSIFPPVLQEATEVKYNASVKCDRM 1021
Db     979 SGVLDCGNCSRIFHGEKLMNTNLIFIMVESKGTCPCDTRLLIQAEQTSDGPN---PCDMV 1035

Qy    1022 RSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNP 1056
Db    1036 KQPRYRKGPDVC--FDNNV-LEDYTDCGGVSGLNP 1067
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RESULT 4
A44147
calcium channel protein alpha-2 chain precursor - rat
N;Alternate names: dihydropyridine-sensitive L-type
N;Contains: calcium channel alpha-2 chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A44147
R;Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992
A;Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensit
A;Reference number: A44147; MUID:92228762; PMID:1314383
A;Accession: A44147
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1091 <KIM>
A;Cross-references: UNIPROT:P54290; GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955
C;Superfamily: calcium channel alpha-2 chain
C;Keywords: calcium; glycoprotein; ion channel; transmembrane protein

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  Query Match            18.5%;  Score 1056.5;  DB 2;  Length 1091;
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  Best Local Similarity   27.6%;  Pred. No. 2.7e-61;
  Matches  308;  Conservative  224;  Mismatches  432;  Indels  151;  Gaps   46;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
              :| | |    ||       ||   |   |: :    :|  :  :||   : |:| :|
Db         33 IKSWVDKMQEDLVTLAKTASGVTQLADIYEKYQDLYTVEPNNARQLVEIAARDIEKLLSN 92

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFD---YYNSVLINERDEKGNFVELGAE-----FL 124
              : :|:  |   ||:    |:: |    :   |||:  :: | : |  | |::     |:
Db         93 RSKALVRLAMEAEKVQAAHQWREDFASNEVVYYNAK--DDLDPERNESESGSQRIKPVFI 150

Qy        125 LESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQY 184
               ::|       ::   ::| :||::|     :|| :  : ||: ||  |   ||| ||
Db        151 EDAN---FGRQISYQHAAVHIPTDIYEGSTIVLNELNWTSALDEVFKRNRDEDPTLLWQV 207

Qy        185 FGSATGFFRIYPGIKWTPDE---NGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGL 241
              | :|    | ||   |  :    | :  :| | | |||| | ||||::||||||||: ||
Db        208 F-AADRLARYYPASPWVDNSRTPNKIDLYDVRRRPWYIQGAASPKDMLILVDVSGSVSGL 266

Qy        242 RMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEEL 301
              : : : ::: :|:|| ::|||: ::|     :  ||:  ||||:  |::  |  |  :
Db        267 TLKLIRTSVSEMLETLSDDDFVNVASFNSNAQDVS-CFQH-LVQANVRNKKVLKDAVNNI 324

Qy        302 MVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKV 361
                ||:    :    ||: |  :  ::    ||: ||| :||  |  : :| |||  | ||
Db        325 TAKGITDYKKGFTFAFEQLLNYNVSRAN--CNKIIMLFTDGGEERAQEIFAKYN-KDKKV 381

Qy        362 RVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHD--H 419
              ||||: :|:       ::|:|| ||||| :| ::   :  |  ||| || ||||:  |
Db        382 RVFTFSVGQHNYDRGPIQWMACENKGYYYEIPSIGAIRINTQEYLDVLGRPMVLAGDKAK 441

Qy        420 DIIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFS----KKNETR-SHGILLGVVGSDVALR 474
              : ||  |:|      |  | |: |  :|||:     :|:|   : ::|||:| ||:|
Db        442 QVQWTNVYLD-------ALELGLVITGTLPVFNVTGQSENKTNLKNQLILGVMGVDVSLE 494

Qy        475 ELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWED 534
              :: :| ||: |  :|| |    |||:| ||:|:|  :  |  :|     ::|  : | |:
Db        495 DIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQP--KNPKSQEPV----TLDFLDAELEN 548

Qy        535 QAE-SLRTAMINRETGTLSMDVKVP------MDKGKRVLFLTNDYFFTDISDTPFSLGAV 587
               :  :|  |||: |:|  :    |       :||| |       | :| :: | :   |:
Db        549 DIKVEIRNKMIDGESGEKTFRTLVKSQDERYIDKGNRT------YTWTPVNGTDYRYLAL 602

Qy        588 LSRGHGEYILLGNTSVEEGL------------HDLLHPD------LALAGDWIYCITDID 629
              :   :  | :     :|| :              : | ||                ||  |:
Db        603 VLPTYSFYYI--KAKIEETITQARSKKGKMKDSETLKPDNFEESGYTFIAPREYC-NDLK 659

Qy        630 PDHRKLSQLEAMIRFLTRKDP-DLECDEELVREVLFDAVVTAPM-EAYWTALALNMSEES 687
              |       |     |: || | :  |: :|:  :| ||  |  : : ||:          :::
Db        660 PSDNNTEFLLNFNEFIDRKTPNNPSCNTDLINRILLDAGFTNELVQNYWS------KQKN 713

Qy        688 EHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAG 747
              |   |: |  |:  |   ::  :     ||      |         |::: ::
Db        714 IKGVKARFVVTDGGITR----VYPKEAGENWQENPETYEDSF--------YKRSLDN--D 759

Qy        748 SFVFNLRW--AEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAAT 805
              ::||   :    || :    ::|  | || : :  :     |  |::: :       |   :
Db        760 NYVFTAPYFNKSGPGAYESGIMV--SKAVELYIQGKLLKPAVVGIKIDVNSWIENFTKTS 817

Qy        806 RQ--CSTVDGPYTQSCEDSD-LDCFVIDNNGFILISKR---SRETGRFLGEVDGAVLTQL 859
              :  |:   ||      :|| :|| ::|: ||:|::     : : ||| ||:|  ::  |
Db        818 IRDPCA---GPVCDCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRFFGEIDPRMMRHL 874

Qy        860 LSMGVFSQVTMYDYQAMCKP------SSHHHSAAQPLVS---PISAFLTATRW-LLQELV 909
              ::: :::    ||||::| |       : | ||  | ::     |  : ||  | :||:|:
Db        875 VNISLYAFNKSYDYQSVCDPGAAPKQGAGHRSAYVPSITDILQIGWWATAAAWSILQQLL 934

Qy        910 LFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPL------QPCDTEYPVFVYQPAIREA 963
              | |          : |  ||  :         ::|         | | ||   : ::   :
Db        935 LSLT--------FPRLLEAVEM--------EEDDFTASLSKQSCITEQTQYFFKNDTKSF 978

Qy        964 NGIVECGPCQKVFVVQQIPNSNLLLLVTDP--TCDCSIFPPVLQEATEVKYNASVKCDRM 1021
              :|:::|| | ::| |::: |:||: :: :   || |     :| :| :   :    || :

Db        979 SGLLDCGNCSRIFHVEKLMNTNLVFIMVESKGTCPCD--TRLLMQAEQTS-DGPDPCDMV 1035

Qy       1022 RSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNP 1056
              :  : |: || |  |   | :|      | |  ||
Db       1036 KQPRYRKGPDVC--FDNNV-LEDYTDCGGVSGLNP 1067


RESULT 5
S44617
C50C3.11 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S44617
R;Favello, A.D.
submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid C50C3.
A;Reference number: S44627
A;Accession: S44617
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-734 <FAV>
A;Cross-references: UNIPROT:P34374; EMBL:L14433; NID:g289649; PID:g289650
C;Genetics:
A;Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

  Query Match             11.2%;  Score 638.5;  DB 2;  Length 734;
  Best Local Similarity   26.6%;  Pred. No. 5.7e-34;
  Matches  180;  Conservative  128;  Mismatches  250;  Indels  119;  Gaps   19;

Qy         10 RDRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENM 69
              :: :|  |       :  | :| |  .:|:: |   |  :: |: |    ::|    :|:
Db         22 KESIKECAKVLSEHMKETFSKISHETILKQNY---EKLVEEEQFDPRAELKKSKHRIEDY 78

Qy         70 LRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLIN--------------ERDEKGN 115
              |: : :       : |   :    |:| | |  :   |                | :  |
Db         79 LKVRSQFAYKAKISLEARSVR---NDSTVNDPQSKSFIRFMSAKQGNDGTTIYESNHLGK 135

Qy        116 FVELG--AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVEN 173
               :::      | |  ||:|  || ::   |:| :|| :|::: |:|  :  |: ::||:  |
Db        136 RLKVNETKSFNLTQNANFYTLPTSSVSSAVHIPTPLYDRNEDLLRKIDWSD-IDAVYRTN 194

Qy        174 FQRDPTLTWQYFGSATGFFRIYPGIKWTPD--ENGVITFDCRNRGWYIQAATSPKDIVIL 231
              :    | :| | |  |: | ||   |  |  :  :  |||||  ||| :||: |:::|:
Db        195 REETKDLAFQLFCSEAGYMRYYPAASWFWDNQDEHLDLFDCRNTEWYINSATNSKNVLIM 254

Qy        232 VDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGI--LVQADRD 289
              :|:|||| | |  :|| |   ||:||  ||: || :: :: | |   |:||
Db        255 LDMSGSMLGQRYEVAKQTTEAILETLSHNDYFNIMTFSKNTFLLDGC-NGTNGLLQATMR 313

Qy        290 NREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEA---KQGSLCNQAIMLISDGAVED 346
              |::  :  ::    :|    ::||  || :|                |   ||||:|||
Db        314 NKKALRRKMDTYQSEGKAEYEKALPLAFSVLLDINNGGGDNNRGACENVIMLITDGAPNA 373

Qy        347 YEPVFEKYNWPDCKVRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYL 406
              |: :|: ||  | ||||||:|:| |    : :: :||||:||   :: :||  | :  |:
Db        374 YKKIFDMYN-ADKKVRVFTFLVGDEAIDFNEVREMACNNRGYMVHVANMADVDEKIHHYI 432

Qy        407 HVLSRPMVINHDHD----IIWTEAYMDS------------------------------ 430
               :|| :|  |  :      ||  | :
Db        433 RRMSR-VVGRHYKESGQLSWWTGVYRERLYLPRPEIFAEPVPITNQSFAVMNKMASRRKI 491

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              :|  |:|:|   :|||: ||     |||       :||   :: | |: : :    :|   |
Db        492 RLQKSEARSRMFVTTVSYPVI--VNET-----FMGVAAVNIPLTEVAQKSHPANIGSKSY 544

Qy        491 AFLNTNNGYILSHPDLRPL-----YREGKKLKPKPNYNSVDLSEVE------------- 531
               |:   ||:::||| |||:      |       | |||::|| |:|
Db        545 FFMLDQNGFVMTHPQLRPIDPFTKYH-------KQNYNNMDLLELEVGQNQNVRSSQKSQ 597

Qy        532 ----------------WEDQAESLRTAMINRETGTL-SMDVKVPMDKGKRVLFLTNDYFF 574
                             :|  :::|  :|: :   :  :||    :   ||   || |:
Db        598 AVSDLVCESGANYAECVDDLRKAVRKMIIDCDNSDVQQLDVLYATELLDRVYPQTNTYYA 657
```

```
Qy        575 TDISDTPPSLGAVLSRG 591
              |:   | ||  :::|
Db        658 ECINHANPVLGLAVAKG 674


RESULT 6
T18770
probable calcium channel protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18770; T25249
R;Sulston, J.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z19019
A;Accession: T18770
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1148 <WIL>
A;Cross-references: UNIPROT:Q17517; EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T2
A;Experimental source: clone B0491
R;Chui, C.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z20004
A;Accession: T25249
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1148 <WI2>
A;Cross-references: EMBL:Z49912; PIDN:CAA90141.1; GSPDB:GN00020; CESP:T24F1.6
A;Experimental source: clone T24F1
C;Genetics:
A;Gene: CESP:T24F1.6
A;Map position: 2
A;Introns: 91/2; 131/3; 170/3; 283/1; 322/2; 410/3; 487/1; 563/1; 602/3; 654/3; 683/3; 7

  Query Match             9.5%;  Score 543;  DB 2;  Length 1148;
  Best Local Similarity   22.3%;  Pred. No. 2.4e-27;
  Matches  247;  Conservative  219;  Mismatches  423;  Indels  218;  Gaps   52;

Qy         25 YNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRRKVEAVQNLVEAA 84
              : | :::|   |:|:::: ::  :| :: |  | :|  :| :: ::  :|:|:: |  :|
Db        120 FETQSRFS---LVQEEFEKLKPDIKSKKEDAAEKLRVATEHLDRLVTNRVDALKKLASSA 176

Qy         85 EEADLNHEFNESLVFDYYN--SVLINERDEKGNFVELGAEFLLESNAHF-SNLPVNTSIS 141
              | :        : ||| |:  :  : : |::    |   : : ||: || ||:  : | |
Db        177 EAS--------AAVFDEYDDQAYAVPQADKR---CEAYMKKMNESDMHFVSNMVEHNSKS 225

Qy        142 SVQLPTNVYNKDPDILNGVYM--SEALNAVFVENFQRDPTLTWQYFGSATGFFRIYPGIK 199
               : :    |  || ::       :: |     :| :: | :  || |: :|  |:||
Db        226 GIHITVESYQCDPRVMRDFDWTGTKHLEKTMSDNKEKAPEMGHQYIGTYSGLTRMYPRRH 285

Qy        200 W--TPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITTILDTL 257
              |   |    :  || | | |:: | : ||||| |:| |||:||  | : | |:  || ||
Db        286 WKVEPTPITIDLFDPRFRPWFVNAESVPKDIVFLLDYSGSVKGPTMHLIKITMMYILSTL 345

Qy        258 GENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVV---DQA-- 312
               ||:   : :|:: : |  |      : |   |:   |:  |||     |::   |||
Db        346 SPNDYFFGVYFNNHFNPIISCANRTFMPATTSNK---KVFFEEL-----GMLEEKDQAHF 397

Qy        313 ---LREAFQILKQFQEAKQG------SLCNQAIMLISDGAVE-DYEPVFEKYNWPDCK-V 361
                 |: :  :|:   :: |       |  :: ::: :||  |  :: : |::   : : :
Db        398 ATPLKFSLDVLRGNLDSNQSLFADYRSEGHKLLIIFTDGVDEWPHQILDEEFQTRNSELI 457

Qy        362 RVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHD--- 418
              |:| : :|   |     :::|| : | |::| :: | :       :|||:   :  |
Db        458 RIFGFSMGYGTSLLPLQQYMACKSHGGYSEIDSIMDVKPQSRTIQNVLSQ---VRGDELK 514

Qy        419 ------HDIIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVA 472
                   :  ||: ||::       |    : |:::|: : :       | |||  |::
Db        515 GTNAEKREPSWTQLYMET-------QGTGPIVTLSLPILTSEQRIWRDQKLAGVVAIDIS 567

Qy        473 LRELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSV------D 526
              ::|  |  |     ::||  :  ||| :: || |:           ||   : |       |
Db        568 IKEFTKHLPTSSEQMYGY--IVDNNGMLIYHPQLQ---------IPKTEVHCVRRSACYD 616

Qy        527 LSEVEWEDQAESLRT------AMINRETG------TLSM-----DVKVPMDKGKRVLFLT 569
               :|: :     ||          : | |      || |     |      |  :|:   |
Db        617 AQQVK-QKAGSGLRVHYGFSDERVYRLVGLIDSIPTLDMYDLEGDSTAIRDLRRRITTKT 675

Qy        570 ----------NDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLLHPDLALAG 619
                       :|  : | ||:||:|           ::: |  ::   :|    :| | |
Db        676 CYEEAIKDNSKEYHCSHIKDSPFTL----------VIVNNIQLKTVYYDDSVQELGLTD 724

Qy        620 D----WIYCITDIDPDHRKLSQLEAMIRF-----LTRKDPDLECDEELVREVLFDAVVTA 670
              :    : |   |:      || :  |  ||     :: |:   : |  | |       |
Db        725 NKLVTFFYPRRDV--CQWKLDEYAAHDRFRVWSDISEKEICAQDDMRLPR------AFTK 776

Qy        671 PMEAY---W--------TALALNMSEESE--HVVDMAFLGTRAGLLRSSLFVGSEKVSDR 717
               : ::   |         | |     | :   | |: :|: ||: |   : | :    |
Db        777 GLGSWTQSWPKSDIEHTTCLLAQYPENASVPHYVN-SFVHTRSKL---TAFYPTCSSHDM 832

Qy        718 KFLTPEDEASVFTLDRFPLWYRQASEHPAGSFV-FNLRWAEGPESAGEPMVVTASTAVAV 776
              | :  : :  :   |                  || |::|          | :::  : |
Db        833 KAVNKKFDEEIKLTDN------------NDFVQFSMR--------SESLLIYRTIA--- 868

Qy        777 TVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFIL 836
              |       | | | |  | : |   |||       |  : |      :| :|  || ::
Db        869 --DYDNNRLAVVGTQWKENFFDQYFDNFTRQ-----NPDWKICRKQ--ECSIITRNGHVI 919

Qy        837 ISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPS--SHHHSAAQPLVSPI 894
              |   |     | : | :   |: : : |  :  : |: ||    :   |||     | :
Db        920 ASSAHRAPAH-LAKFDPQLFESLVKVNLVSTNSWTEVQSECKAKRVAPWSSAAPGSSSIL 978

Qy        895 SAFLTATRWLLQELVLFLLEWSVWGSWYDRG---AEAK-SVFHHSHKHKKQDPLQPCDTE 950
               |:|:        :  | : | | :  :      :|: |:  ::   :|  | : | :
Db        979 RYFVTS--------IFKLAKTSFWRNLLESALTLVDAQPSMTGNTCTFQKIKPFERCFMK 1030

Qy        951 YPVFVYQPAIR-----EANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQ 1005
              :  | |:  :       :  |:  |    |::   :|:: | |:: |    || : |  :
Db       1031 F--FHYRMTLNITKQLQLTGMSTCSRYAKLY---PVPHTTLSLIIADRA--CSQYRP--K 1081

Qy       1006 EATEVKYNASVKCDRMRSQKLRRRPDS 1032
                | :     ||| : |   |||||:
Db       1082 RIFESEPRKLEKCDVVHSH-ARRRPDA 1107


RESULT 7
C86880
hypothetical protein yvcC [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86880
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86880
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1450 <STO>
A;Cross-references: UNIPROT:Q9CE07; GB:AE005176; PID:g12725093; PIDN:AAK06141.1; GSPDB:GN
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yvcC
C;Superfamily: uncharacterized conserved protein with vWa domain

  Query Match             3.7%;  Score 209.5;  DB 2;  Length 1450;
  Best Local Similarity   18.5%;  Pred. No. 3.8e-05;
  Matches  198;  Conservative  162;  Mismatches  345;  Indels  363;  Gaps   51;

Qy         38 QKKYKDVESSLKIEEVDGLELVRKFS-EDMENMLRRKVEAVQNLVEAAEEADLNHEF--- 93
              || |||     |:| ::       :| : :||    :::    |  |  :|  |   |
Db         33 QKNYKD-----KVELINDESFNISYSMQALENQYEWEIDYRINKTENDKELKLKFSFEGN 87

Qy         94 -------NESLVFDYYNSVLIN-ERDEKGNFV-----------ELGAEF-LLESNAHFS 132
                    |||       |::: : |:: :|  |           |: |:  |:|::
Db         88 QPIEIEENESWTLKEKNTIISDFEKENEGKIVLRANNSISLLNLEIQADAKLIENDQEVI 147
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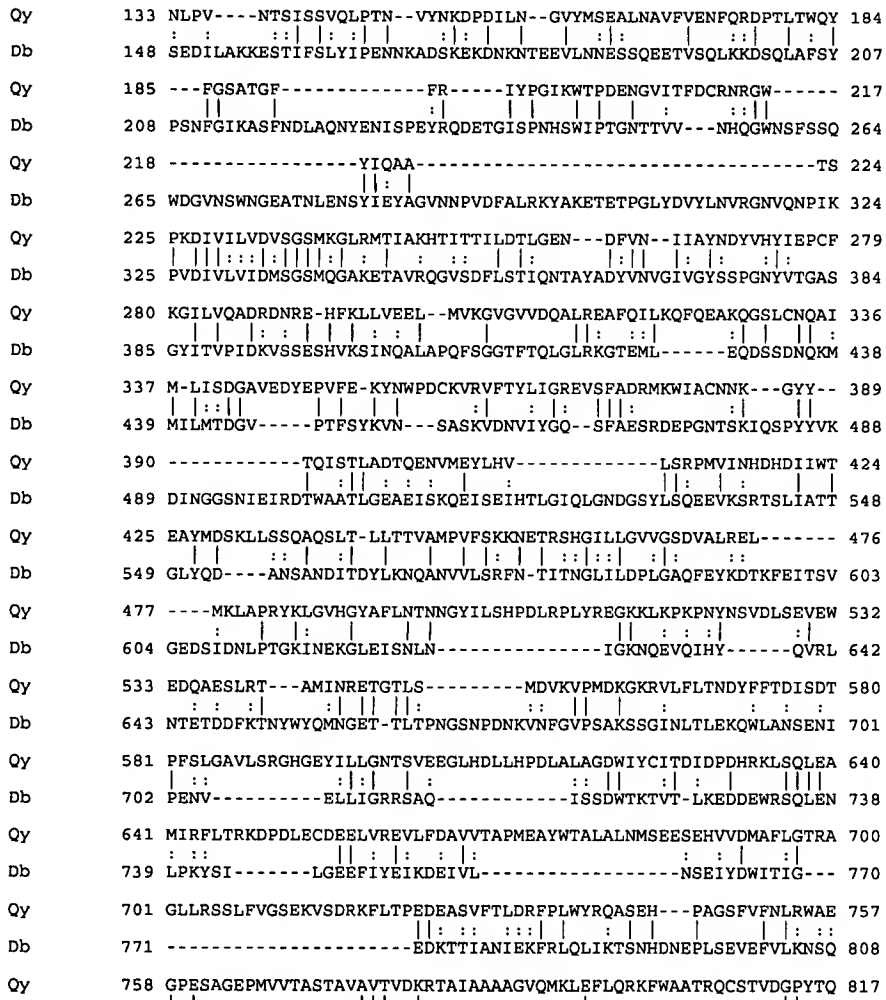

RESULT 8
IYHU2
inter-alpha-trypsin inhibitor heavy chain 2 precursor - human
N;Alternate names: inter-alpha-trypsin inhibitor complex component II
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00346; S09064; B39967; S00632; B34245; S28929; C53642

R;Gebhard, W.; Schreitmueller, T.; Hochstrasser, K.; Wachter, E.
FEBS Lett. 229, 63-67, 1988
A;Title: Complementary DNA and derived amino acid sequence of the precursor of one of the
A;Reference number: S00346; MUID:88152237; PMID:2450046
A;Accession: S00346
A;Molecule type: mRNA
A;Residues: 1-946 <GEB>
A;Cross-references: UNIPROT:P19823; EMBL:X07173
A;Experimental source: liver
A;Note: part of this sequence, including the amino end of the mature protein, was confirm
ssing occurs at the carboxyl as well as the amino end to produce the mature protein
A;Note: due to a double frameshift, the nucleic acid sequence of codons 363-372 is incons
A;Note: in one clone, a T is lacking from codon 716; this clone could code for a protein
R;Schreitmueller, T.; Hochstrasser, K.; Reisinger, P.W.M.; Wachter, E.; Gebhard, W.
Biol. Chem. Hoppe-Seyler 368, 963-970, 1987
A;Title: cDNA cloning of human inter-alpha-trypsin inhibitor discloses three different pr
A;Reference number: S09064; MUID:88024442; PMID:3663330
A;Accession: S09064
A;Molecule type: mRNA
A;Residues: 265,'RR',268-284,'D',286-946 <SCH>
A;Note: this sequence has been revised in reference S00346
R;Salier, J.P.; Diarra-Mehrpour, M.; Sesboue, R.; Bourguignon, J.; Benarous, R.; Ohkubo,
Proc. Natl. Acad. Sci. U.S.A. 84, 8272-8276, 1987
A;Title: Isolation and characterization of cDNAs encoding the heavy chain of human inter-
A;Reference number: A39967; MUID:88068576; PMID:2446322
A;Accession: B39967
A;Molecule type: mRNA
A;Residues: 384-673,'A',675-704,'S',706-728,'D',730,'A',732-865 <SAL>
A;Cross-references: GB:M18193; GB:J03013; NID:g338222; PIDN:AAA60558.1; PID:g553647
A;Experimental source: liver
R;Salier, J.P.; Diarra-Mehrpour, M.; Sesbouee, R.; Bourguignon, J.; Martin, J.P.
Biol. Chem. Hoppe-Seyler 369(Suppl.), 15-18, 1988
A;Title: Human inter-alpha-trypsin inhibitor. Isolation and characterization of heavy (H)
A;Reference number: S00632; MUID:89076497; PMID:2462430
A;Accession: S00632
A;Molecule type: mRNA
A;Residues: 384-673,'A',675-704,'S',706-728,'D',730,'A',732-766 <SA2>
A;Cross-references: GB:M33033; NID:g186589; PIDN:AAA59195.1; PID:g186590
R;Enghild, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.
J. Biol. Chem. 264, 15975-15981, 1989
A;Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-alp
A;Reference number: A92736; MUID:89380192; PMID:2476436
A;Accession: B34245
A;Molecule type: protein
A;Residues: 55-74 <ENG>
R;Malki, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fournet
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
A;Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation,
A;Reference number: S28928; MUID:93039735; PMID:1384548
A;Accession: S28929
A;Molecule type: protein
A;Residues: 55-64 <MAL>
R;Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
Biochemistry 33, 7423-7429, 1994
A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comple
A;Reference number: A53642; MUID:94271799; PMID:7516184
A;Accession: C53642
A;Molecule type: protein
A;Residues: 55-64 <WIS>
C;Comment: Inter-alpha-trypsin inhibitor is a complex of three proteins, each deriving fr
C;Comment: This protein is a heterodimer of heavy and light chains.
C;Genetics:
A;Gene: GDB:ITIH2
A;Cross-references: GDB:120108; OMIM:146640
A;Map position: 10p15-10p15
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
C;Keywords: carboxyglutamic acid; glycoprotein; heterodimer; serine proteinase inhibitor
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-54/Domain: propeptide #status predicted <PRO>
F;55-698/Product: inter-alpha-trypsin inhibitor heavy chain 2 #status predicted <MAT>
F;96,445/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;118,671/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;282,283/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted

```
F;421,422,423/Binding site: calcium (Asp, Gly, Asp) #status predicted

  Query Match             3.1%;  Score 175;  DB 1;  Length 946;
  Best Local Similarity   18.6%;  Pred. No. 0.0036;
  Matches  158;  Conservative  122;  Mismatches  296;  Indels  272;  Gaps   36;

Qy         58 LVRKFSEDMENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFV 117
              |||  : ||||  | :|    |  |  : :|:::  :       |   :  :       :
Db        154 LVRSSALDMEN-FRTEVNV---LPGAKVQFELHYQEVKWRKLGSYEHRIYLQPGRLAKHL 209

Qy        118 EL--------GAEFLLESN---AHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEAL 166
              |:        |  ||   :   ||  :||   ||  |   :|  |
Db        210 EVDVWVIEPQGLRFLHVPDTFEGHFDGVPV---ISKGQQKAHVSFK------------- 252

Qy        167 NAVFVENFQRDPTLTWQYFGSATGFFRIYPGIKWTP-DENGVITFDCRN----------R 215
                      ||:  |          || |  :  |   |: :| :
Db        253.-----------PTVAQQ---------RICPSCRETAVDGELVVLYDVKREEKAGELEVFN 292

Qy        216 GWYIQAATS------PKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYN 269
              |:::           ||:|: ::|||||| |::|       : |||| |    |  ::| :|
Db        293 GYFVHFFAPDNLDPIPKNILFVIDVSGSMWGVKMKQTVEAMKTILDDLRAEDHFSVIDFN 352

Qy        270 DYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQG 329
               :      ::  |: | :       |  :|::   |   :::||  |  ||    ||
Db        353 QNIR----TWRNDLISATKTQVADAKRYIEKIQPSGGTNINEALLRAIFIL---NEANNL 405

Qy        330 SLCN----QAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREVSFADRMKWIACNN 385
              | :      |:|:|||      :|                    :| |:  :   |
Db        406 GLLDPNSVSLIILVSDG-----DPT-----------------VG-ELKLSKIQK------ 436

Qy        386 KGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKLLSSQAQSLTLLTT 445
                     : :||: : : : :|  |  : |:|
Db        437 -----------NVKENIQDNISLFSLGMGFDVDYD------------------------ 460

Qy        446 VAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAFLNTNNGYILSHPD 505
                   | |:    :|||   : |:     :| |              | |      :| |
Db        461 -----FLKRLSNENHGIAQRIYGNQDTSSQLKK-------------FYNQ-----VSTPL 497

Qy        506 LRPL------------------YREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINR 546
              || :                |  | ::     ::   | ::|    | | |  | ::
Db        498 LRNVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGKFDPAKLDQIESVITATSANTQLV-L 556

Qy        547 ETGTLSMDVKVPMDKGKRV---------LFLTNDYFFTDISDTPFSLG------AVLSRG 591
              ||      |::  : | |              :|| :    :  | |  :         ::|
Db        557 ETLAQMDDLQDFLSKDKHADPDFTRKLWAYLTINQLLAERSLAPTAAAKRRITRSILQMS 616

Qy        592 HGEYILLGNTSV--------EEGLHDLLHPDLALAGDWIYCITDIDPDHRK--------- 634
                 :|:   ||:        |  | |    | :     :|  : : ||
Db        617 LDHHIVTPLTSLVIENEAGDERMLADAPPQDPSCCSGALYYGSKVVPDSTPSWANPSPTP 676

Qy        635 -LSQLEAMIRFLTRKDPD----LECDEELVREVLFDAVVTAPMEAYWTALALNMSEESEH 689
               :| |    : |     |     :| |            ::  |       :  |:  |
Db        677 VISMLAQGSQVLESTPPPHVMRVENDPHF--------IIYLPKSQ--KNICFNIDSEPGK 726

Qy        690 VVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLT----------PED---EASVFTLDRFPL 736
              ::::      :|:: :   ||::| :: |  |             ||   | |  |:
Db        727 ILNLV-SDPESGIVVNGQLVGAKKPNNGKLSTYFGKLGFYFQSEDIKIEISTETI----- 780

Qy        737 WYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTA--STAVAVTVDKRTAIAAAAGVQMKL 794
                    |  ||  |:| |::  :   : : ::      | :|:||          :|
Db        781 ----TLSH--GSSTFSLSWSDTAQVTNQRVQISVKKEKVVTITLDK----------EMSF 824

Qy        795 EFLQRKFW 802
                |  : |
Db        825 SVLLHRVW 832


RESULT 9
JC5575
inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5575; PC4485
R;Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
J. Biochem. 122, 71-82, 1997
A;Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors
sin inhibitor heavy chain family.
A;Reference number: JC5574; MUID:97420688; PMID:9276673
A;Accession: JC5575
A;Molecule type: mRNA
A;Residues: 1-946 <NAK>
A;Cross-references: UNIPROT:P97279; DDBJ:D89286; NID:g1694689; PIDN:BAA13939.1; PID:g169
A;Experimental source: liver
A;Accession: PC4485
A;Molecule type: protein
A;Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>
C;Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 wer
 that the complexes play important role for panceatic cancer.
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
F;261-264,717-916/Disulfide bonds: #status predicted

  Query Match             3.0%;  Score 172.5;  DB 2;  Length 946;
  Best Local Similarity   23.3%;  Pred. No. 0.0052;
  Matches   90;  Conservative   60;  Mismatches  126;  Indels  111;  Gaps   18;

Qy        117 VEL-GAEFLLESN---AHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVE 172
              ||| |  ||   :    ||  :||   ||  |  ::|  |
Db        216 VELQGMRFLHVPDTFEGHFQGVPV---ISKGQKKSHVSFK------------------- 252

Qy        173 NFQRDPTLTWQYFGSATGFFRIYPGIKWTP-DENGVITFDCRN----------RGWYIQA 221
                    ||:  |          |  |   :|  |   |: :|               |:::
Db        253 -----PTVAQQ---------RKCPNCTYTAVDGELVVMYDVNREEKVGELEVFNGYFVHF 298

Qy        222 ATS------PKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYI 275
                    ||:|: ::|||||| |::|       : |||| |    |  ::: :|  |
Db        299 FAPENLDPIPKNILFVIDVSGSMWGIKMKQTVEAMKTILDDLRTEDQFSVVDFNHNVR-- 356

Qy        276 EPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQGSLCN-- 333
                 ::  || | :       |  :|::   |   :::||  |  ||    ||    : |
Db        357 --TWRNDLVSATKTQITDAKRYIEKIQPSGGTNINEALLRAIFIL---NEASNLGMLNPD 411

Qy        334 --QAIMLISDGAVEDYEPVF-----------EKYNWPDCKVRVFTYLIGREVSFADRMKW 380
                   |:|:|||      :|               | |  |  : :|:  || :| : | :|
Db        412 SVSLIVLVSDG-----DPTVGELKLSKIQKNVKQNIQD-NISLFSLGIGFDVDY-DFLKR 464

Qy        381 IACNNKGYYTQISTLADTQENVMEYLHVLSRPMVIN------------------HDH--- 419
                  ::  |:|   :|    ||   : :: : :| |:: |                  |::
Db        465 LSNENRGIAQRIYGNRDTSSQLKKFYNQVSTPLLRNVQFNYPQASVTDVTQNSFHNYFGG 524

Qy        420 -DIIWTEAYMDSKLLSSQAQSLTLLTT 445
               :|:    |  |||  :: ||:   |:
Db        525 SEIVVAGKYDPSKL--AEVQSIITATS 549


RESULT 10
S54354
inter-alpha-inhibitor H2 chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54354
R;Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.
Biochem. J. 306, 505-512, 1995
A;Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse:
A;Reference number: S54353; MUID:95194326; PMID:7534067
A;Accession: S54354
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-946 <CHA>
A;Cross-references: UNIPROT:Q61703; EMBL:X70392; NID:g695633; PIDN:CAA49842.1; PID:g6956
C;Superfamily: inter-alpha-trypsin inhibitor complex component II

  Query Match             2.9%;  Score 166.5;  DB 2;  Length 946;
  Best Local Similarity   23.4%;  Pred. No. 0.013;
  Matches   62;  Conservative   52;  Mismatches   84;  Indels   67;  Gaps    9;

Qy        225 PKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILV 284
```

```
Db        308 PKNILFVIDVSGSMWGIKMKQTVEAMKTILDDLRTDDQFSVVDFNHNVR----TWRNDLV 363

Qy        285 QADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQGSLCN----QAIMLIS 340

Db        364 SATKTQIADAKRYIEKIQPSGGTNINEALLRAIFIL---NEASNMGLLNPDSVSLIILVS 420

Qy        341 DG------------------AVEDYEPVFEKYNWPDCKVRVFTYLIGREVSFADRMKWIA 382

Db        421 DGDPTVGELKLSKIQKNVKQSIQD-------------NISLFSLGIGFDVDY-DFLKRLS 466

Qy        383 CNNKGYYTQISTLADTQENVMEYLHVLSRPMVIN------------------HDH----D 420

Db        467 NENRGIAQRIYGNQDTSSQLKKFYNQVSTPLLRNVQFNYPQASVTDVTQNNFHNYFGGSE 526

Qy        421 IIWTEAYMDSKLLSSQAQSLTLLTT 445

Db        527 IVVAGKFDPSKL--TEVQSIITATS 549


RESULT 11
JX0368
inter-alpha-trypsin inhibitor heavy chain-related protein precursor - human
N;Alternate names: IHRP; plasma glycoprotein
C;Species: Homo sapiens (man)
C;Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JX0368; PC2355; S68457; S78548
R;Saguchi, K.; Tobe, T.; Hashimoto, K.; Sano, Y.; Nakano, Y.; Miura, N.H.; Tomita, M.
J. Biochem. 117, 14-18, 1995
A;Title: Cloning and characterization of cDNA for inter-alpha-trypsin inhibitor family h
A;Reference number: JX0368; MUID:95293915; PMID:7775381
A;Accession: JX0368
A;Molecule type: mRNA
A;Residues: 1-930 <SAG1>
A;Cross-references: UNIPROT:Q14624; DDBJ:D38595; NID:g664887; PIDN:BAA07602.1; PID:g1483
A;Accession: PC2355
A;Molecule type: protein
A;Residues: 29-44;48-55;61-75;99-111;140-151;163-169;211-224;246-267;274-281;296-329;392
A;Experimental source: liver
R;Nishimura, H.; Kakizaki, I.; Muta, T.; Sasaki, N.; Pu, P.X.; Yamashita, T.; Nagasawa,
FEBS Lett. 357, 207-211, 1995
A;Title: cDNA and deduced amino acid sequence of human PK-120, a plasma kallikrein-sensi
A;Reference number: S68457; MUID:95104473; PMID:7805892
A;Accession: S68457
A;Molecule type: mRNA
A;Residues: 1-84,'I',86-113,'S',115-930 <NIS>
A;Cross-references: EMBL:D38535; NID:g624879; PIDN:BAA07536.1; PID:g1402590
A;Accession: S78548
A;Molecule type: protein
A;Residues: 29-45;171-184;211-239;274-281;301-315;429-443;488-502;690-695;697-700;703-72
A;Experimental source: liver
C;Comment: The amino-terminal 600 residues exhibits homology with those of inter-alpha t
C;Function:
A;Description: highly sensitive to plasma kallikrein
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; serine proteinase inhibitor
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-687/Product: inter-alpha trypsin inhibitor heavy chain-related protein #status pred
F;688-930/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;81,207,517,577/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;666/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F;696,702/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;701/Binding site: carbohydrate (Thr) (covalent) #status predicted

  Query Match             2.9%;  Score 164.5;  DB 2;  Length 930;
  Best Local Similarity   19.0%;  Pred. No. 0.017;
  Matches  147;  Conservative  118;  Mismatches  313;  Indels  195;  Gaps   31;

Qy         26 NTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSE--------------DMENML 70

Db         62 NTVQEATFQMELPKKAFITNFSMNIDGMTYPGIIKEKAEAQAQYSAAVAKGKNAGLVKAT 121

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130

Db        122 GRNMEQFQVSVSVAPNAKITFE----LVYE----ELLKRR--------LGVYELL----- 160

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190

Db        161 ---LKVRPQQLVKHLQMDIHIFEP---QGISFLET-ESTFMTNQLVDALTTWQ--NKTKA 211

Qy        191 FFRIYPGI----------KWTPDENGVITFDCR----------NRGWYIQ------AATS 224

Db        212 HIRFKPTLSQQQKSPEQQETVLDGNLIIRYDVDRAISGGSIQIENGYFVHYFAPEGLTTM 271

Qy        225 PKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILV 284

Db        272 PKNVVFVIDKSGSMSGRKIQQTREALIKILDDLSPRDQFNLIVFSTEATQWRPS----LV 327

Qy        285 QADRDNREHFKLLVEELMVKGVGVVDQALREAFQIL---KQFQEAKQGSLCNQAIMLISD 341

Db        328 PASAENVNKARSFAAGIQALGGTNINDAMLMAVQLLDSSNQEERLPEGSV--SLIILLTD 385

Qy        342 G--AVEDYEPVFEKYNWPDC---KVRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLA 396

Db        386 GDPTVGETNPRSIQNNVREAVSGRYSLFCLGFGFDVSYAFLEK-LALDNGGLARRIHEDS 444

Qy        397 DTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNE 456

Db        445 DSALQLQDFYQEVANPLL------TAVTFEYPSNAVEEVTQNNFRLLFKGSEMVVAGKLQ 498

Qy        457 TRSHGILLGVVG------------SDVALRELMKLAPRY-------KLGVH-------- 488

Db        499 DRGPDVLTATVSGKLPTQNITFQTESSVAEQEAEFQSPKYIFHNFMERLWAYLTIQQLLE 558

Qy        489 ----------------------GYAFLNTNNGYILSHPD--------LRPL--------- 509

Db        559 QTVSASDADQQALRNQALNLSLAYSFVTPLTSMVVTKPDDQEQSQVAEKPMEGESRNRNV 618

Qy        510 ---------YREGKKL-KPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLS---MDVK 556

Db        619 HSGSTFFKYYLQGAKIPKPEASFS----PRRGWNRQAGAAGSRM-NFRPGVLSSRQLGLP 673

Qy        557 VPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLLHPD-- 614

Db        674 GPPDVPDHAAY----HPFRRLAILPASAPPATSNPDPAVSRVMNMKIEETTMTTQTPAPI 729

Qy        615 ------LALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVRE 661

Db        730 QAPSAILPLPGQSVERLC-VDPRHR-----QGPVNLLSDPEQGVEVTGQYERE 776


RESULT 12
JC5576
inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C;Accession: JC5576; PC4486
R;Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
J. Biochem. 122, 71-82, 1997
A;Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors
sin inhibitor heavy chain family.
A;Reference number: JC5574; MUID:97420688; PMID:9276673
A;Accession: JC5576
A;Molecule type: mRNA
A;Residues: 1-889 <NAK>
A;Cross-references: DDBJ:D89287
A;Experimental source: liver
A;Accession: PC4486
A;Molecule type: protein
A;Residues: 34-53;449-475;509-526 <NA2>
C;Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were
 that the complexes play important role for panceatic cancer.
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
F;236-239,664-865/Disulfide bonds: #status predicted

  Query Match             2.6%;  Score 150.5;  DB 2;  Length 889;
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```
  Best Local Similarity   22.7%;  Pred. No. 0.13;
  Matches   64;  Conservative   58;  Mismatches  111;  Indels   49;  Gaps   10;

Qy        225 PKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILV 284
              ||:|| ::|:|||| | ::   :  :  ||| : ::|::| | ::  |      :|  ||
Db        282 PKNIVFVIDISGSMAGRKIQQTRVALLKILDDMKQDDYLNFILFSTGV----TTWKDSLV 337

Qy        285 QADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQA---IMLISD 341
              ||   | |  :  |  :  :|:  ::  |    ::|   :|  | ::  ::   |::::|
Db        338 QATPANLEEARTFVRSISDQGMTNINDGLLRGIRMLTDARE--QHTVPERSTSIIIMLTD 395

Qy        342 GAVEDYEPVFEKYNWPDCKVRVFTYLIGR----EVSFADRMKW-----IACNNKGYYTQI 392
              |      |   ||      :  |   : ||     : | : : :     :|  | |   :|
Db        396 GDANTGESRPEK-----IQENVRKAIEGRFPLYNLGFGNNLNYNFLETMALENHGVARRI 450

Qy        393 STLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFS 452
              :|    :  :   :: |:: | : :       | :: :|          ||  : | |
Db        451 YEDSDANLQLQGFYEEVANPLLTNVEVE------YPENAILD--------LTKNSYPHFY 496

Qy        453 KKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAFLN 494
              :||   | |     ||:           :|  | |:  ||
Db        497 DGSETAVAGRL---ADSDM---------NNFKADVKGHGALN 526


RESULT 13
S54355
inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54355
R;Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.
Biochem. J. 306, 505-512, 1995
A;Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse:
A;Reference number: S54353; MUID:95194326; PMID:7534067
A;Accession: S54355
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-886 <CHA>
A;Cross-references: UNIPROT:Q61704; EMBL:X70393; NID:g695635; PIDN:CAA49843.1; PID:g6956
C;Superfamily: inter-alpha-trypsin inhibitor complex component II

  Query Match             2.6%;  Score 148.5;  DB 2;  Length 886;
  Best Local Similarity   22.5%;  Pred. No. 0.18;
  Matches   63;  Conservative   61;  Mismatches  111;  Indels   45;  Gaps    9;

Qy        225 PKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILV 284
              ||:|| ::|||||| | ::   :  :  ||| : |:|::| | ::  |      :|  ||
Db        279 PKNIVFVIDVSGSMSGRKIQQTREALLKILDDVKEDDYLNFILFSTDV----TTWKDHLV 334

Qy        285 QADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQE-----AKQGSLCNQAIMLI 339
              ||   | :  |  |: :  : :  ::  | :  ::| : :|      :  |:    |::
Db        335 QATPANLKEAKTFVKNIHDQSMTNINDGLLKGIEMLNKAREDHTVPERSTSI----IIML 390

Qy        340 SDGAVEDYEPVFEKY-----NWPDCKVRVFTYLIGREVSFADRMKWIACNNKGYYTQIST 394
              :||     |   ||      |    | ::    |  ::: : :: :|  | |   :|
Db        391 TDGDANTGESRPEKIQENVRNAIGGKFPLYNLGFGNNLNY-NFLETLALENHGLARRIYE 449

Qy        395 LADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKK 454
              :|    :  :   :: |:: | : :      | :: :|          ||  : | |
Db        450 DSDANLQLQGFYEEVANPLLTNVEVE------YPENAILD--------LTRNSYPHFYDG 495

Qy        455 NETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAFLN 494
              :|         :|   || | : :    :|  | |:  ||
Db        496 SE---------IV---VAGRLVDRNMDNFKADVKGHGALN 523


RESULT 14
S30350
inter-alpha-trypsin inhibitor heavy chain 3 precursor - human
N;Alternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-alpha-inhibitor heav
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S30350; S34123; S02141; D34245; A39079; S50133; B53642; A59167
R;Bourguignon, J.; Diarra-Mehrpour, M.; Thiberville, L.; Bost, F.; Sesbouee, R.; Martin,
Eur. J. Biochem. 212, 771-776, 1993
A;Title: Human pre-alpha-trypsin inhibitor-precursor heavy chain cDNA and deduced amino-
A;Reference number: S30350; MUID:93215656; PMID:7681778
A;Accession: S30350
A;Molecule type: mRNA
A;Residues: 1-885 <BOU1>
A;Cross-references: UNIPROT:Q06033; EMBL:X67055; NID:g288562
R;Bourguignon, J.
submitted to the EMBL Data Library, June 1992
A;Reference number: S34123
A;Accession: S34123
A;Molecule type: mRNA
A;Residues: 1-310,'K',312-343,'R',345-885 <BOU2>
A;Cross-references: EMBL:X67055; NID:g288562; PIDN:CAA47439.1; PID:g288563
R;Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Mattei, M.G.; Passage, E.; Salier,
Eur. J. Biochem. 179, 147-154, 1989
A;Title: Human plasma inter-alpha-trypsin inhibitor is encoded by four genes on three ch
A;Reference number: S02141; MUID:89137072; PMID:2465147
A;Accession: S02141
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 341-356,'G',358-845,'H',847-885 <DIA1>
A;Cross-references: EMBL:X14690; NID:g35464; PIDN:CAA32821.1; PID:g35465
R;Enghild, J.J.; Thogersen, I.B.; Pizzo, S.V.; Salvesen, G.
J. Biol. Chem. 264, 15975-15981, 1989
A;Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
A;Reference number: A92736; MUID:89380192; PMID:2476436
A;Accession: D34245
A;Molecule type: protein
A;Residues: 30-49 <ENG1>
R;Enghild, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherfurd, S.; Pizzo, S.V.
J. Biol. Chem. 266, 747-751, 1991
A;Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot
A;Reference number: A39079; MUID:91093267; PMID:1898736
A;Accession: A39079
A;Molecule type: protein
A;Residues: 631-647 <ENG2>
R;Diarra-Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesbouee, R.; Muschio-Bon
Biochim. Biophys. Acta 1219, 551-554, 1994
A;Title: Tandem orientation of the inter-alpha-trypsin inhibitor heavy chain H1 and H3 g
A;Reference number: S50132; MUID:95002176; PMID:7522574
A;Accession: S50133
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <DIA2>
A;Cross-references: EMBL:X75318
R;Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
Biochemistry 33, 7423-7429, 1994
A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comple
A;Reference number: A53642; MUID:94271799; PMID:7516184
A;Accession: B53642
A;Molecule type: protein
A;Residues: 30-34,'X' <WIS>
R;Jessen, T.E.; Faarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A;Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a no
A;Reference number: S02431; MUID:88167187; PMID:2450785
A;Accession: A59167
A;Molecule type: protein
A;Residues: 30-32,'GEKEQAVDT' <JES>
C;Comment: As pre-alpha-inhibitor, this protein is covalently cross-linked by chondroitin
C;Genetics:
A;Gene: GDB:ITIH3
A;Cross-references: GDB:120109; OMIM:146650
A;Map position: 3p13-3p12
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; heterodimer; proteinase inhi
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-29/Domain: propeptide #status predicted <PRO>
F;30-647/Product: inter-alpha-trypsin inhibitor heavy chain 3 #status experimental <MAT>
F;648-885/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;87,576/Binding site: carbohydrate (Asn) (covalent) #status predicted
```

```
F;647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #stat

  Query Match             2.6%;  Score 146.5;  DB 2;  Length 885;
  Best Local Similarity   21.9%;  Pred. No. 0.24;
  Matches   73;  Conservative   63;  Mismatches  147;  Indels   51;  Gaps   14;

Qy        118 ELGAEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDIL--NGVYMSEALNAVFVENFQ 175
              ||  | ||:   |    :  :   ||  : :  : ||    |: | :|  | |: |
Db        149 ELTYEELLK--RHKGKYEMYLKVQPKQLVKH-FEIEVDIFEPQGISMLDA-EASFITNDL 204

Qy        176 RDPTLTWQYFGSATGFFRIYPGIKWTPDE-----------NG--VITFDCRN------- 214
                || : |    |     | :    |:             ||   ||:|
Db        205 LGSALT-KSFSGKKGHVSFKPSL----DQQRSCPTCTDSLLNGDFTITYDVNRESPGNVQ 259

Qy        215 --RGWYIQ------AATSPKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNII 266
                |:::          ||::  ::|:|||| | ::   |  :  ||: : | |::| |
Db        260 IVNGYFVHFFAPQGLPVVPKNVAFVIDISGSMAGRKLEQTKEALLRILEDMQEEDYLNFI 319

Qy        267 AYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGV-GVVDQALREAFQILKQFQE 325
              ::  |      :|  |||| :| :  |  |: :  ||:  : |  ||    : |  :|
Db        320 LFSGDV----STWKEHLVQATPENLQEAKTFVKSMEDKGMTNINDGLLRGISMLNKAREE 375

Qy        326 AKQGSLCNQAIMLISDGAVEDYEPVFEKY-----NWPDCKVRVFTYLIGREVSFADRMKW 380
              :        :::::||      |   ||      |    | ::    |  ::: : ::
Db        376 HRIPERSTSIVIMLTDGDANVGESRPEKIQENVRNAIGGKFPLYNLGFGNNLNY-NFLEN 434

Qy        381 IACNNKGYYTQISTLADTQENVMEYLHVLSRPMV 414
              :|  | |:  :|   :|    :  :  :: |::
Db        435 MALENHGFARRIYEDSDADLQLQGFYEEVANPLL 468


RESULT 15
A90551
conserved hypothetical protein MYPU_3130 [imported] - Mycoplasma pulmonis (strain UAB CT
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A90551
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: A90551
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2819 <KUR>
A;Cross-references: UNIPROT:Q98QP8; GB:AL445566; PID:g14089727; PIDN:CAC13486.1; GSPDB:G
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_3130
A;Genetic code: SGC3

  Query Match             2.5%;  Score 145.5;  DB 2;  Length 2819;
  Best Local Similarity   18.7%;  Pred. No. 1.9;
  Matches  154;  Conservative  130;  Mismatches  261;  Indels  279;  Gaps   41;

Qy         41 YKDVESSLKIEEVDGLELVRK----FSEDMENMLRRKVEAVQ--NLVEAAEEADLN-HEF 93
              : :|  :| :  ||  ||: |    | |::::  : |:   :  ||:|  ::: ::   |
Db        733 FYEVSKTL-VNIVDTEELLEKVLKNFIEEIKSSAQLKLSNPKEFNLIEKLQKSIISTFGF 791

Qy         94 NESLVFDYYNSVL-------INERDEKGNFVELGAEFLLESNAHFSNL--PVNTSISSVQ 144
                | :  |:        : :||:  : ::    |: :|    : |     | :|:::
Db        792 TNDLGWSFLKQVVKSKSLSSVEQRDKFTSSLKEVVSFVFKSENVKNKLISSAGTYLSNIE 851

Qy        145 LPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTL----------TWQYFGSATGFFRI 194
              |    : :: |:  |::         : ||:: | |          :|:        |
Db        852 L----FKENSDVFKGIFS-------HILNFEKTPELLNKIIDYVINSWESIDQYNDAFEF 900

Qy        195 YPGIKWTPDENGVITFDCRNRGWYIQAATSPKDI---VILVDVS-----------GSMK 239
                      |: |   |  |:    |  |||   |:  ::              |
Db        901 -----------VLNFLKTNSSWF---KTYVKDIFSSVVNSEIQYANILTSKLNKLASQA 945

Qy        240 GLRMT----------------IA-KHTITTILD------TLGENDFVNIIAYNDYVHYI 275
              |  :|                ||  :||  ::|      || | |  | ||

Db        946 GFELTNSSVESIKNIFTNTLKIIADSNTIDALVDTFVNSKTLLEIDKKNFIA-------- 997

Qy        276 EPCFKGILVQADRDNR--EHFKLLVEELMVKGVGVVDQALREAFQILKQ--FQEAKQGSL 331
                | | : |  |:     || |:    :|    |:|  ::   :||:  |:|
Db        998 --SLKNIQIFALSDDNFFSVFKALISSNKLKDKAFVNQYKQDITNVLKELLFEE------ 1049

Qy        332 CNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR-----EVSFADRMKWIACNNK 386
                :   ||   :     :||  | |:   :  | |          :  | ::|  |  :|
Db       1050 --KFFNLIYSFMMPKTSELFE--NNPEALNKTTTILRNALKKNLDPDFINKMMDIIFDNL 1105

Qy        387 GYYTQIST--------LADTQENVMEYLHVLSRPMVINHD-HDII------WTEAYMDSK 431
                | ::          | |  : :   :  : : :|   :  |::       |: :|  :
Db       1106 DKYQKLENYGQVLGLILKDNSDAIATKVQAIFKDVVNEANFQDVLKVLLVSQTKKFMGFE 1165

Qy        432 LLSSQAQSL-TLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              | : :   : | || :   ||   |  :|                  : || :  | : |
Db       1166 LNADETNKISTDLTKILKQVFESNNFAKS----------------LALATKDSLVIDGV 1208

Qy        491 ----------AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSV----DLSEVEWEDQA 536
                       ||||   ::||  |           | | ||  |    :   ::    :
Db       1209 QANKKIFDFTRFLNT---FLLSEKD----------EKTKENYQMVKSILNTKLIDISQNS 1255

Qy        537 ESLRTAMINRETGTLSMD------VKVPMDKGKRVLFLTNDYFF----------TDISD- 579
              ||::  :       || |      :|| : | |      |  | |           |: ||
Db       1256 ESIKNLLKTFTKSALSRDEFYEKTIKVFLSKEKLASAYTPVYEFVKFVLKNEKTTNFSDL 1315

Qy        580 ------TPFS-------------------------------------------LGAVLS- 589
                    ||                                           ||  ::
Db       1316 LIDSLFKDFSQYQQANSFEELIYLVLRNNKETVVNYLKELSFEIKSSNIIQRLLGQTINA 1375

Qy        590 --RGHGEYI-----------------LLGNTSVEEGLHDLLHPDLALAGDWIYCITDID 629
                  :|| |                 | | |::   |:||:   |:: :    :| ::
Db       1376 LVTPNGEKIFSDTELQSLSTLINESLDLFGKTNIISNLYDLVLSALSINQESSSVLTKVE 1435

Qy        630 P-DHRKLSQLE---AMIR-FLTRKDPDLECDEELVREVLFDAVV 668
                |: | |      |:|:  |: |: |::  :|       | |::
Db       1436 NITHKALDQQNSYFAVIKTLLSVKEGDVDKSDE------FKAII 1473


Search completed: November 16, 2005, 03:24:34
Job time : 54 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 16, 2005, 03:12:42 ; Search time 188 Seconds
(without alignments)
2968.970 Million cell updates/sec

Title: US-09-833-222A-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTPVPVLLGGNIRVYAL 1090

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5399.5	94.3	1120	2	Q8IZS9	Q8izs9 homo sapien
2	5373.5	93.8	1137	2	Q7Z3S7	Q7z3s7 homo sapien
3	4649	81.2	974	2	Q7Z3S8	Q7z3s8 homo sapien
4	3422	59.8	1091	2	Q9Z1L5	Q9z1l5 mus musculu
5	3416.5	59.7	1091	2	Q8IZS8	Q8izs8 homo sapien
6	3410	59.6	1085	2	Q8CFG5	Q8cfg5 rattus norv
7	3250.5	56.8	997	2	Q9NY16	Q9ny16 homo sapien
8	1866.5	32.6	519	2	Q9NY18	Q9ny18 homo sapien
9	1551	27.1	1218	2	Q9V6T7	Q9v6t7 drosophila
10	1496.5	26.1	1170	2	Q8IP22	Q8ip22 drosophila
11	1441	25.2	2190	2	Q9VJM0	Q9vjm0 drosophila
12	1430.5	25.0	1028	2	Q7Q758	Q7q758 anopheles g
13	1398	24.4	1011	2	Q7PM00	Q7pm00 anopheles g
14	1305.5	22.8	1255	2	Q9NK83	Q9nk83 drosophila
15	1283	22.4	1120	2	Q9VJN7	Q9vjn7 drosophila
16	1262	22.0	394	2	Q8AVY7	Q8avy7 xenopus lae
17	1243	21.7	967	2	Q7PM11	Q7pm11 anopheles g
18	1189	20.8	1098	2	Q8CHE9	Q8che9 mus musculu
19	1183.5	20.7	1076	2	Q9UEW0	Q9uew0 homo sapien
20	1183.5	20.7	1145	2	Q9Y268	Q9y268 homo sapien
21	1182.5	20.7	1157	2	Q8CFG6	Q8cfg6 rattus norv
22	1182	20.6	1084	2	Q920H6	Q920h6 mus musculu
23	1182	20.6	1156	2	Q9EQG2	Q9eqg2 mus musculu
24	1180	20.6	1148	2	Q8C8R8	Q8c8r8 mus musculu
25	1174.5	20.5	1143	2	Q9NY48	Q9ny48 homo sapien
26	1173	20.5	1154	2	Q6PHS9	Q6phs9 mus musculu
27	1171.5	20.5	1186	2	Q6REE3	Q6ree3 mus musculu
28	1171	20.5	1150	2	Q9NY47	Q9ny47 homo sapien
29	1109	19.4	1084	2	Q8CFG7	Q8cfg7 rattus norv
30	1106.5	19.3	1103	1	CIC2_MOUSE	O08532 mus musculu
31	1105.5	19.3	1091	2	Q9ERS3	Q9ers3 rattus norv
32	1101.5	19.2	1079	2	Q8VHS9	Q8vhs9 rattus norv
33	1090	19.0	1091	2	O77773	O77773 sus scrofa
34	1089	19.0	975	2	Q7Z6Z1	Q7z6z1 homo sapien
35	1089	19.0	1106	1	CIC2_RABIT	P13806 oryctolagus
36	1078	18.8	1110	2	Q9UIU0	Q9uiu0 homo sapien
37	1077.5	18.8	1091	1	CIC2_HUMAN	P54289 homo sapien
38	1056.5	18.5	1091	1	CIC2_RAT	P54290 rattus norv
39	949.5	16.6	204	2	Q86XZ5	Q86xz5 homo sapien
40	935.5	16.3	842	2	Q95R75	Q95r75 drosophila
41	705	12.3	1249	1	UN36_CAEEL	P34374 caenorhabdi
42	672.5	11.7	745	2	Q9UDQ3	Q9udq3 homo sapien
43	543	9.5	1067	2	Q17517	Q17517 caenorhabdi
44	543	9.5	1067	2	Q7JMF9	Q7jmf9 caenorhabdi
45	452	7.9	140	2	Q8JFR4	Q8jfr4 brachydanio

ALIGNMENTS

RESULT 1
Q8IZS9
ID Q8IZS9 PRELIMINARY; PRT; 1120 AA.
AC Q8IZS9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Voltage-gated calcium channel alpha(2)delta-4 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22169250; PubMed=12181424;
RA Qin N., Yagel S., Momplaisir M.L., Codd E.E., D'Andrea M.R.;
RT "Molecular cloning and characterization of the human voltage-gated calcium channel alpha(2)delta-4 subunit.";
RL Mol. Pharmacol. 62:485-496(2002).
DR EMBL; AF516695; AAN06672.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
SQ SEQUENCE 1120 AA; 126204 MW; 4F950C11C3249984 CRC64;

Query Match 94.3%; Score 5399.5; DB 2; Length 1120;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1035; Conservative 5; Mismatches 11; Indels 3; Gaps 2;

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Qy          11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
               : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy          71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy         131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy         191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy         251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         298 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy         311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 657

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 777

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 837

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 897

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 957

Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 1017

Qy        971 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1030
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1077

Qy       1031 DSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
                 |||||||||   : | | |  :| :|  | | :|
Db       1078 DSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1110


RESULT 2
Q7Z3S7
ID   Q7Z3S7      PRELIMINARY;      PRT;  1137 AA.
AC   Q7Z3S7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein DKFZp686O0495.
GN   Name=DKFZp686O0495;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human retina;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX537437; CAD97679.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 2.
DR   Pfam; PF00092; VWA; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   1137 AA;  127965 MW;  69410B72580F3FF7 CRC64;

  Query Match           93.8%;  Score 5373.5;  DB 2;  Length 1137;
  Best Local Similarity   97.8%;  Pred. No. 1.6e-317;
  Matches 1031;  Conservative    5;  Mismatches   15;  Indels    3;  Gaps    2;

Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 134

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 194

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 254

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 314

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 374

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 434

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 494

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 554

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 614

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        615 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 674

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        675 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLARKDPDLECDEELVREVLFDAVVTA 734

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        735 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 794

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        795 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 854

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        855 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 914

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        915 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 974
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Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        975 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECE 1034

Qy        971 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1035 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1094

Qy       1031 DSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
              |||||||||   : | | |  :| :|  | | :|
Db       1095 DSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1127


RESULT 3
Q7Z3S8
ID   Q7Z3S8      PRELIMINARY;      PRT;   974 AA.
AC   Q7Z3S8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein DKFZp686A1395.
GN   Name=DKFZp686A1395;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human retina;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX537436; CAD97678.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 2.
DR   Pfam; PF00092; VWA; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   974 AA;  109568 MW;  6F3C91CD0A038ED2 CRC64;

  Query Match             81.2%;  Score 4649;  DB 2;  Length 974;
  Best Local Similarity   99.4%;  Pred. No. 1.3e-273;
  Matches  895;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 134

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 194

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 254

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 314

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        315 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVNGVGVVD 374

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 434

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 494

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 554

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 614

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        615 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 674

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        675 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 734

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        735 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 794

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        795 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 854

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        855 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 914

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        915 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 974


RESULT 4
Q9Z1L5
ID   Q9Z1L5      PRELIMINARY;      PRT;  1091 AA.
AC   Q9Z1L5;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Calcium channel alpha-2-delta-C subunit.
GN   Name=Cacna2d3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;
RT   "Molecular diversity of the calcium channel alpha2delta subunit.";
RL   J. Neurosci. 19:648-691(1999).
DR   EMBL; AJ010949; CAA09423.1; -.
DR   PIR; T30256; T30256.
DR   MGD; MGI:1338890; Cacna2d3.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 2.
DR   Pfam; PF00092; VWA; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
SQ   SEQUENCE   1091 AA;  122777 MW;  7AEE2BDA10077A0A CRC64;

  Query Match             59.8%;  Score 3422;  DB 2;  Length 1091;
  Best Local Similarity   60.0%;  Pred. No. 5.5e-199;
  Matches  627;  Conservative  188;  Mismatches  212;  Indels   18;  Gaps    6;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
              |||||  |||:: :   ||||| |||||||: |  : |||:|||:|||:| :: || |  :
Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKIMEEMFHK 101
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Qy        73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
Db       102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy       133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
Db       162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy       193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
Db       222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy       253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
Db       282 ILDTLGDDDFFNIITYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy       313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
Db       342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy       373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
Db       402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy       433 LSSQA----QSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVH 488
Db       462 PQAQKLADDQGLVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLGIH 521

Qy       489 GYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRET 548
Db       522 GYAFAITNNGYILTHPELRPLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNRKT 580

Qy       549 GTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLH 608
Db       581 GKFSMEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEGLH 640

Qy       609 DLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVV 668
Db       641 DLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVV 700

Qy       669 TAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASV 728
Db       701 SAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENI 760

Qy       729 FTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAA 788
Db       761 FNADHFPLWYRRAAEQIAGSFVYSIPFSTG--TVNKSNVVTASTSIQLLDERKSPVVAAV 818

Qy       789 GVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFL 848
Db       819 GIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFF 878

Qy       849 GEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQEL 908
Db       879 GEVEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDSAHGLLDPYKAFLSAAKWIMTEL 938

Qy       909 VLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVE 968
Db       939 VLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIA 990

Qy       969 CGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRR 1028
Db       991 CEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKIRR 1050

Qy      1029 RPDSCHAFHPEVRVEADRGWAGFSS 1053
Db      1051 RPESCHGFHPE---ENARECGGASS 1072


RESULT 5
Q8IZS8
ID   Q8IZS8      PRELIMINARY;      PRT;  1091 AA.
AC   Q8IZS8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Voltage-gated calcium channel alpha(2)delta-3 subunit.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22169250; PubMed=12181424;
RA   Qin N., Yagel S., Momplaisir M.L., Codd E.E., D'Andrea M.R.;
RT   "Molecular cloning and characterization of the human voltage-gated
RT   calcium channel alpha(2)delta-4 subunit.";
RL   Mol. Pharmacol. 62:485-496(2002).
DR   EMBL; AF516696; AAN06673.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 2.
DR   Pfam; PF00092; VWA; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
SQ   SEQUENCE   1091 AA;  123010 MW;  4E5E50BD38F05082 CRC64;

  Query Match             59.7%;  Score 3416.5;  DB 2;  Length 1091;
  Best Local Similarity   60.3%;  Pred. No. 1.2e-198;
  Matches  623;  Conservative  188;  Mismatches  203;  Indels   19;  Gaps    6;

Qy        13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
Db        42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKNMEEMFHK 101

Qy        73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
Db       102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy       133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
Db       162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy       193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
Db       222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy       253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
Db       282 ILDTLGDDDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy       313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
Db       342 LNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFTYLIGREA 401

Qy       373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
Db       402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy       433 LSSQAQSLT------LLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLG 486
Db       462 --PQAQKLTDDQGPVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLG 519

Qy       487 VHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINR 546
Db       520 IHGYAFAITNNGYILTHPELRLLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNR 578

Qy       547 ETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEG 606
Db       579 KTGKFSMEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRGNVTIEEG 638

Qy       607 LHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDA 666
Db       639 LHDLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDA 698
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Qy        667 VVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEA 726
              ||:||:|||||:|||| || |:  |::|||||| || | :||||:|::::: ||    |:
Db        699 VVSAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKE 758

Qy        727 SVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAA 786
              ::|  | ||||||:|:|   ||||::: :: ||    :  ||||||:: :  :::: : |
Db        759 NIFNADHFPLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVVA 816

Qy        787 AAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGR 846
              | |:|||||| ||||| |:|||:::||  : ||:|  ::|::|||||||:|:   :||
Db        817 AVGIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGD 876

Qy        847 FLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQ 906
              | ||::|||: :||:|| | ::|:|||||||: :      |  |: | :|||:| :|::
Db        877 FFGEIEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPYNAFLSAVKWIMT 936

Qy        907 ELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGI 966
              ||||||:|:::  ||:     ||:        | :  |:|||||| || :  |:|  |
Db        937 ELVLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGN 988

Qy        967 VECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKL 1026
              : |  | | ||:||||:||| ::| | :| |    |:     |::|| |:||:|:::||:
Db        989 IACEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKI 1048

Qy       1027 RRRPDSCHAFHPE 1039
              ||||:||| ||||
Db       1049 RRRPESCHGFHPE 1061
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RESULT 6
Q8CFG5
ID Q8CFG5 PRELIMINARY; PRT; 1085 AA.
AC Q8CFG5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium channel alpha-2 delta-3 subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Atrium;
RX MEDLINE=22494975; PubMed=12606261; DOI=10.1016/S0022-2828(02)00313-9;
RA Chu P.J., Best P.M.;
RT "Molecular cloning of calcium channel alpha(2)delta-subunits from rat
RT atria and the differential regulation of their expression by IGF-1.";
RL J. Mol. Cell. Cardiol. 35:207-215(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Atrium;
RA Chu P.-J., Best P.M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF486278; AAO14654.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
SQ SEQUENCE 1085 AA; 122203 MW; 9584F533E318002A CRC64;

Query Match 59.6%; Score 3410; DB 2; Length 1085;
Best Local Similarity 59.8%; Pred. No. 2.9e-198;
Matches 622; Conservative 191; Mismatches 212; Indels 16; Gaps 6;

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Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRR 72
              |||||  |||:: :   |||||:|||||||: |  : |||:|||:||:| :::|| |  :
Db         42 VKLWASAFGGEIKSIAAKYSGSQLLQKKYKEYEKDVAIEEIDGLQLVKKLAKNMEEMFHK 101

Qy         73 KVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
              | |||: |||||||| | |||:  | ::|:|:|||||||: |||:||| ||:|  | ||:
Db        102 KSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFILAPNDHFN 161

Qy        133 NLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFF 192
              ||||| |:| ||:|||:||||| |:|||| ||:|| |||:|| |||:| ||||||| |||
Db        162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYFGSAKGFF 221

Qy        193 RIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITT 252
              | |||||| ||||||| |||||| |||||||||||:|||||||||||||:|||| |:::
Db        222 RQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTIAKQTVSS 281

Qy        253 ILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQA 312
              ||||||::|| ||| ||: :||:|||  | |||||  |:|||:  :::|  ||:|::| |
Db        282 ILDTLGDDDFFNIITYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIA 341

Qy        313 LREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREV 372
              | ||| :|  |     |||:|:||||||:||||: |: :| |||||: |||:|||||||
Db        342 LNEAFNVLSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPERKVRIFTYLIGREA 401

Qy        373 SFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKL 432
              :||| :||:|| |||::|||||||| |||||||||||||| ||: :||::|||||:|| |
Db        402 AFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTEAYIDSTL 461

Qy        433 LSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAF 492
              :  | | |:|||||||||:|||||  ||||||||:|| ::||:|  |:||||:|||||
Db        462 --ADDQGLVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKLGIHGYAF 519

Qy        493 LNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLS 552
              |||||||:||:||||| |||| : ||||:|||||||||||: : || ||:||:||  |
Db        520 AITNNGYILTHPELRPLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVNRKTGKFS 578

Qy        553 MDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLLH 612
              |:||  :|||||| :||||::|||  |||||  |||||:|    || ::|||||| |
Db        579 MEVKKTVDKGKRVLVMTNDYYYTDIKGAPFSLGVALSRGHGKYFFRGNVTIEEGLHDLEH 638

Qy        613 PDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAPM 672
              ||::|| :| || ||: |:|| |||||:  :|  |:| |:||:||::|||||||:||:
Db        639 PDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELIQEVLFDAVVSAPI 698

Qy        673 EAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLD 732
              |||||:|||| || |:  |::|||||| || | :||||:|::::: ||    |: ::|  |
Db        699 EAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKARDKENIFNAD 758

Qy        733 RFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQM 792
              ||||||:|:|   ||||::: :: |  :  :  ||||||:: :  :::: : || |:||
Db        759 HFPLWYRRAAEQIPGSFVYSIPFSTG--TVNKSNVVTASTSIQLLDERKSPVVAAVGIQM 816

Qy        793 KLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEVD 852
              |||| ||||| |:|||:::||  : ||:|  ::|::|||||||:|:   :|| | |||:
Db        817 KLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYTQTGDFFGEVE 876

Qy        853 GAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFL 912
              |||: :||:|| | ::|:|||||||: :     :|  |: |  |||:| :|:: ||||||
Db        877 GAVMNKLLTMGSFKRITLYDYQAMCRANKESSDSAHGLLDPYKAFLSAAKWIVTELVLFL 936

Qy        913 LEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECGPC 972
              :|:::  ||:     ||:        | :  |:|||||| || :  |:|  | : |  |
Db        937 VEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERTIKETTGNIACEDC 988

Qy        973 QKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRPDS 1032
              | ||:|||||||| ::| | :| |    |:     |::|| |:||:|:::||:||||:|
Db        989 SKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKIRRRPES 1048

Qy       1033 CHAFHPEVRVEADRGWAGFSS 1053
              || ||||   |  |   | ||
Db       1049 CHGFHPE---ENARECGGASS 1066
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RESULT 7
Q9NY16
ID Q9NY16 PRELIMINARY; PRT; 997 AA.
AC Q9NY16;

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DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Calcium channel alpha2-delta3 subunit.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21142395; PubMed=11245980; DOI=10.1016/S0378-1119(00)00600-4;
RA   Hanke S., Bugert P., Chudek J., Kovacs G.;
RT   "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT   tumor suppressor gene region at chromosome 3p21.1 in conventional
RT   renal cell carcinoma.";
RL   Gene 264:69-75(2001).
DR   EMBL; AJ272268; CAB75962.1; -.
DR   Genew; HGNC:15460; CACNA2D3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 2.
DR   Pfam; PF00092; VWA; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
SQ   SEQUENCE   997 AA;  112996 MW;  B56D13133FD67B8D CRC64;

  Query Match           56.8%;  Score 3250.5;  DB 2;  Length 997;
  Best Local Similarity  60.5%;  Pred. No. 1.3e-188;
  Matches  593;  Conservative  177;  Mismatches  191;  Indels   19;  Gaps    6;

Qy         66 MENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLL 125
              ||  |   :|  |||: ||||||||  | |||:  | ::|:|:|||||||: |||:||| ||:|
Db          1 MEEMFHKKSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFIL 60

Qy        126 ESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYF 185
                | ||:||||| |:|  ||:|||:||||| |:|||| ||:|| |||:|| ||||:| ||||
Db         61 APNDHFNNLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYF 120

Qy        186 GSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTI 245
              ||| |||| |||||| ||||||| |||||| ||||||||||:|||||||||||||:||
Db        121 GSAKGFFRQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTI 180

Qy        246 AKHTITTILDTLGENDFVNIIAYNDYVVHYIEPCFKGILVQADRDNREHFKLLVEELMVKG 305
              || |:::|||||::|| |||||: :||:|||  | |||||| |:|||:  :::|  ||
Db        181 AKQTVSSILDTLGDDDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKG 240

Qy        306 VGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFT 365
              :|::| || ||| ||  |    |||:|:|||||:|||: |: :| |||||| |||:||
Db        241 IGMLDIALNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFT 300

Qy        366 YLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTE 425
              |||||| :||| :||:|| |||::|||||||| |||||||||||||| ||: :||::|||
Db        301 YLIGREAAFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTE 360

Qy        426 AYMDSKLLSSQAQSLT------LLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKL 479
              ||:|| |   ||| ||      |:|||||||||:|||| |||||||:|| ::||:|
Db        361 AYIDSTL--PQAQKLTDDQGPVLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKT 418

Qy        480 APRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESL 539
              |:||||:|||||  |||||||:||:|| || |||| : ||||:|||||||||||: : |
Db        419 IPKYKLGIHGYAFAITNNGYILTHPELRLLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVL 477

Qy        540 RTAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLG 599
              | ||:||:||  ||:||  :|||||| :||||::|||  ||||||  |||||:|   |
Db        478 RNAMVNRKTGKFSMEVKKTVDKGKRVLVMTNDYYYTDIKGTPFSLGVALSRGHGKYFFRG 537

Qy        600 NTSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELV 659
              | ::||||||| |||::|| :| || ||: |:|| ||||||:  :|  |:| |:||:||:
Db        538 NVTIEEGLHDLEHPDVSLADEWSYCNTDLHPEHRHLSQLEAIKLYLKGKEPLLQCDKELI 597

Qy        660 REVLFDAVVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKF 719
              :|||||||:||:|||||:|||| || |:  |::|||||| || | :||||:|:::::: |
Db        598 QEVLFDAVVSAPIEAYWTSLALNKSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDF 657

Qy        720 LTPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVD 779
              |    |: ::|  | ||||||:|:|   ||||::: :: ||    :  ||||||:: :  :
Db        658 LKAGDKENIFNADHFPLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDE 715

Qy        780 KRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISK 839
              ::: : || |:|||||| |||||  |:|||:::||  : ||:|  ::|::|||||||:|:
Db        716 RKSPVVAAVGIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSE 775

Qy        840 RSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLT 899
                 :|| | ||::|||: :||:|| | ::|:|||||||: :      |  |: | :|||:
Db        776 DYTQTGDFFGEIEGAVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPYNAFLS 835

Qy        900 ATRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPA 959
              | :|:: ||||||:|::: ||:     ||:         | :  |:|||||| || :
Db        836 AVKWIMTELVLFLVEFNLC-SWWHSDMTAKA-------QKLKQTLEPCDTEYPAFVSERT 887

Qy        960 IREANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCD 1019
              |:|  | : |  | | ||:||||:||| ::| | :| |    |:     |::|| |:||:
Db        888 IKETTGNIACEDCSKSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCE 947

Qy       1020 RMRSQKLRRRPDSCHAFHPE 1039
              |:::||:||||:||| ||||
Db        948 RLKAQKIRRRPESCHGFHPE 967


RESULT 8
Q9NY18
ID   Q9NY18      PRELIMINARY;      PRT;   519 AA.
AC   Q9NY18;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Calcium channel alpha2-delta3 subunit.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=21142395; PubMed=11245980; DOI=10.1016/S0378-1119(00)00600-4;
RA   Hanke S., Bugert P., Chudek J., Kovacs G.;
RT   "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT   tumor suppressor gene region at chromosome 3p21.1 in conventional
RT   renal cell carcinoma.";
RL   Gene 264:69-75(2001).
DR   EMBL; AJ272213; CAB75878.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 1.
DR   Pfam; PF00092; VWA; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
SQ   SEQUENCE   519 AA;  59526 MW;  198D13AF246286C6 CRC64;

  Query Match           32.6%;  Score 1866.5;  DB 2;  Length 519;
  Best Local Similarity  68.9%;  Pred. No. 6.1e-105;
  Matches  344;  Conservative   71;  Mismatches   81;  Indels    3;  Gaps    2;

Qy         66 MENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLL 125
              ||  |   :|  |||: ||||||||  | |||:  | ::|:|:|||||||: |||:||| ||:|
Db          1 MEEMFHKKSEAVRRLVEAAEEAHLKHEFDADLQYEYFNAVLINERDKDGNFLELGKEFIL 60

Qy        126 ESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYF 185
                | ||:||||| |:|  ||:|||:||||| |:|||| ||:|| |||:|| ||||:| ||||
Db         61 APNDHFNNLPVNISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRDPSLIWQYF 120

Qy        186 GSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTI 245
              ||| |||| |||||| ||||||| |||||| ||||||||||:|||||||||||||:||
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Db        121 GSAKGFFRQYPGIKWEPDENGVIAFDCRNRKWYIQAATSPKDVVILVDVSGSMKGLRLTI 180

Qy        246 AKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKG 305
              || |:::|||||::|| |||||: :||:|||  | |||||| |:|||:  :::|  ||
Db        181 AKQTVSSILDTLGDDDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHFREHLDKLFAKG 240

Qy        306 VGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFT 365
              :|::| || ||| ||  |    |||:|:||||||:||||: |: :| |||||| |||:||
Db        241 IGMLDIALNEAFNILSDFNHTGQGSICSQAIMLITDGAVDTYDTIFAKYNWPDRKVRIFT 300

Qy        366 YLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTE 425
              |||||| :||| :||:|| |||::|||||||| |||||||||||||| ||: :||::|||
Db        301 YLIGREAAFADNLKWMACANKGFFTQISTLADVQENVMEYLHVLSRPKVIDQEHDVVWTE 360

Qy        426 AYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKL 485
              ||:|| |   |     |:|||||||||:||||| |||||||:|| ::||:|  |:|||
Db        361 AYIDSTLTDDQGP--VLMTTVAMPVFSKQNETRSKGILLGVVGTDVPVKELLKTIPKYKL 418

Qy        486 GVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMIN 545
              |:|||||  |||||||:||:|| || |||| : ||||:||||||||||: : || ||:|
Db        419 GIHGYAFAITNNGYILTHPELRLLYEEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMVN 477

Qy        546 RETGTLSMDVKVPMDKGKR 564
              |:||  ||:|| .:||| |
Db        478 RKTGKFSMEVKKTVDKGFR 496
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RESULT 9
Q9V6T7
ID   Q9V6T7      PRELIMINARY;      PRT;  1218 AA.
AC   Q9V6T7; Q8T9C3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   CG12295-PB (SD07723p).
GN   ORFNames=CG12295;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003817; AAF58335.2; -.
DR   EMBL; AY069830; AAL39975.1; -.
DR   FlyBase; FBgn0033870; CG12295.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 2.
DR   Pfam; PF00092; VWA; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
SQ   SEQUENCE   1218 AA;  140048 MW;  4F04224063D527B5 CRC64;

  Query Match             27.1%;  Score 1551;  DB 2;  Length 1218;
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  Best Local Similarity   33.0%;  Pred. No. 3.2e-85;
  Matches  397;  Conservative  207;  Mismatches  365;  Indels  234;  Gaps   43;

Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEV---DGLELVRKFSEDMENM 69
              |  |||   | :|:     : |  : ::  |:|: | |  :|   :|  :|   :::| |
Db         40 VHSWADKLGMELF-----HLGDFITRR--KEVQESFKDAKVVSRNGASIVDSMAKEIEMM 92

Qy         70 LRRKVEAVQNLVEAAEEADLNHEFN-ESLVFDYYNSVLINERDEKGNFV----------- 117
              :  || ||: ::: ||   |:|: :   :| ||::    |  | |: |
Db         93 MDLKVSAVRRIMDTAENTALSHQNDMADKMFSYYSA---KEMLEPGDPVPPIPTPAPDMD 149

Qy        118 -ELGAEFL--------LESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNA 168
               ::|   :         ||    | | ||| |:||| :| ||::: ||::  :  || |:
Db        150 KDIGEPLIYVQPKVVVLEPRPEFHNTPVNFSVSSVHVPVNVFDRAPDVIKAIQWSENLDQ 209

Qy        169 VFVENFQRDPTLTWQYFGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDI 228
              :| :|:: ||||:||:|||:||| | :|  ||  |   |  :||| | ||::|||||||
Db        210 IFRDNYKNDPTLSWQFFGSSTGFMRQFPASKWRKDV-PVDLYDCRLRSWYMEAATSPKDI 268

Qy        229 VILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADR 288
              |||:| |||| | |: |||| : ||||||| ||||||  ::  |  : |||:  |:||:
Db        269 VILMDGSGSMLGQRLDIAKHVVNTILDTLGTNDFVNIFTFDKEVSPVVPCFEDTLIQANL 328

Qy        289 DNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYE 348
              |    |  :|    | :     || :|||::|:: : : :|: ||||||:| ||| |:
Db        329 GNIRELKEGIELFRPKSIANYTAALTKAFELLEETKLSSRGAQCNQAIMIIGDGAPENNR 388

Qy        349 PVFEKYNW---PDCKVRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEY 405
              ||| :||   |   |||||||||:|||:  | ::|:|| |:|||  :|  |: :| |: |
Db        389 EVFELHNWRDPPYKPVRVFTYLIGKEVANWDDIRWMACENQGYYVHLSDTAEVREMVLNY 448

Qy        406 LHVLSRPMVI-NHDHDIIWTEAYMD----------------------------SKLLS 434
              : |::||:|:  ||| :||:: | |                            ::|
Db        449 IPVMARPLVLGRHDHPVIWSQVYADIEDTKLSDYLWDINQCEYQKADVLEYWQVHDRMLE 508

Qy        435 S------------------QAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRE 475
                               :     :|||:||:: ::         :||| |:|| : |
Db        509 PSEMHRRKYRRMKETWNQPVDSNVYQFMTTVSMPIYDRRENATRIANILGVAGTDVPINE 568

Qy        476 LMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQ 535
              : ||   : |||:|||: |||||:| ||| ||:: :|  |||   |||||: |||  |
Db        569 IKKLLSPFTLGVNGYAFIVTNNGYVLFHPDFRPIF-QGYILKPA--YNSVDMIEVELLDD 625

Qy        536 AE----------SLRTAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLG 585
                        ::| ::||: ||:  | ||    |: |||  :   |::| |  |||:|
Db        626 DRPARDFNPVLMTIRDSIINQSTGSKWMLVKNHFDEMKRVARVKRQYYWTAIKKTPFTLV 685

Qy        586 AVLSRGHG------------EYILLGNT---SVEEGLHDLLHPDLALAGDWIYCITDIDP 630
                  :|               | :  |   ||  |    :||      ||::|
Db        686 ISYPEQYGVSHMDIRADQEIHRISIKGTNLRSVFSGKRWKIHP------DWLFC------ 733

Qy        631 DHR----KLSQLEAMIRFLTRKD--------------PD----LECDEELVREVLFDAVV 668
              |      |  ::| :: || |                |:    : || :|:: ::||| |
Db        734 KHSNRTFKTPEIE-LLYFLERMSEPGWRWPGSRSAMPPEHAAAMFCDRQLMQALVFDARV 792

Qy        669 TAPMEAYWTA--LALNMSEESEHV------VDMAFLGTRAGLLRSSLF---VGSEKVSDR 717
              |       | :   : |  ::  :       | :||| | :|| |    |       |
Db        793 TG-----WFSNNTSFNSKDDKGNEFKQRFGVTVAFLATHSGLTRWHEFHSNAAEESGVGE 847

Qy        718 KFLTPEDEASVFTLDRFPLWYRQA-SEH--PAGSFVFNLRWAEGPESAGE---PMVVTAS 771
              |     : :   :|   :||::|  :|     |||:::     |  |||    ::||||
Db        848 TF----SQNNTRAIDE--IWYKRAVDQHFVREESFVYSV-----PFDAGESNSEILVTAS 896

Qy        772 TAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDN 831
              ||      :|| ||  | | :    | : |    |      ||          | ||:::||
Db        897 HAVFHNEGGKTAPAAVVGFQFQHSALYKLFHNITGNACAVD----------DKDCYILDN 946

Qy        832 NGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLV 891
              ||:::|| |  ||||| |||:||:: :||   |: |||:|||||:|  | : ::|:  |:
Db        947 NGYVIISTRVHETGRFFGEVNGAIMKRLLEENVYRQVTVYDYQAVCFESKNDNNASSMLL 1006

Qy        892 SPISAFLTATRWLLQELVLF---LLEWS--VWGSWYDRGAEAKSV---------FHHSHK 937
              ||:   |   :|||   : :   ||:|:  |   : |   ::             ||:

Db       1007 SPLFHLLRVGKWLLHTALWYIVQLLQWAPGVSSHYADMYGDSNDTEPPPPEPHPDHHARN 1066

Qy        938 ---HKKQDP------------LQPCDTEYPVFVYQPAIREANGIV---ECGPCQKVFVV 978
                  | |:|               |:||| :  ::       | : :|       |:: |||
Db       1067 GNGHGKKDDDHWLRYLTLHRTRLKPCDMKRDLYT---LFNEKDNVVYNMTAHACERPFVV 1123

Qy        979 QQIPNSNLLLLVTDPTC--DCSIFPPVLQEATE--VKYNASVKCDRMRSQKLRRRPDSCH 1034
                 || |||:||| |  |  | |:   |  :  :  :  | |: | :   :  | || ||
Db       1124 LPIPFSNLILLVIDQLCPRDGSVVLTVNPQPIDYHLSVNDSLACYKQAREFNRMRPHSCI 1183

Qy       1035 AFH 1037
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Db       1184 SRH 1186
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RESULT 10
Q8IP22
ID   Q8IP22   PRELIMINARY;   PRT; 1170 AA.
AC   Q8IP22;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CG12455-PB.
GN   ORFNames=CG12455;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;

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RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003650; AAN10933.1; -.
DR   FlyBase; FBgn0028859; CG12455.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 1.
DR   Pfam; PF00092; VWA; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
SQ   SEQUENCE   1170 AA;  135684 MW;  3F566259715FA761 CRC64;

  Query Match           26.1%;  Score 1496.5;  DB 2;  Length 1170;
  Best Local Similarity  32.6%;  Pred. No. 6.2e-82;
  Matches  387;  Conservative  200;  Mismatches  417;  Indels  183;  Gaps   42;

Qy         16 WADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRRKVE 75
              ||  || :|:    | : |  :::|||  | : ::|  :| ||::  ::::  || ||::
Db         13 WATQFGDELFALAQKITKSQEIKEKYK--EYNARVELKNGTELIKSITKNVGRMLARKMD 70

Qy         76 AVQNLVEAAEEADLNHEFNESLV---FDYYNSVLI----NERDE----KGNFVELGAEFL 124
              ||: : | ||  : | ||| :     | |::|       |  :|    :  |  :
Db         71 AVRCIQERAEYVNENFEFNLTYALQNFTYFSSKYSTFNGNSSEELEPNEAEFAWMYRNME 130

Qy        125 LESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQY 184
              |  : || | ||:|  ||| :|:|::::   :|  :  || |: || :|:| || |:|||
Db        131 LNPDTHFYNTPVDTEHSSVHVPSNIWDRSERVLKTIMWSEHLDEVFRQNYQSDPALSWQY 190

Qy        185 FGSATGFFRIYPGIKWT---PDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGL 241
              ||| ||  | ||  :||   |: :   |:||| | |||: ||  ||||||:| |||| |
Db        191 FGSDTGILRHYPAAQWTDTRPNRDDADTYDCRKRSWYIETATCSKDIVILLDHSGSMTGF 250

Qy        242 RMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEEL 301
              |  :|| || :|||   |||  |: |:  |: | ||| | ||||  :| | |   :|:|
Db        251 RHHVAKFTIRSILDTFSNNDFFTILRYSSEVNDIIPCFNGALVQATPENIEVFNQQIEQL 310

Qy        302 -MVKGVGVVDQALREAFQILKQFQEAKQ---GSLCNQAIMLISDGAVEDYEPVFEKYNW- 356
               :|   :  |   |||:|::: :::     | |||||||::||   :   ||:||||
Db        311 DDPEGYANLTLAYETAFQLLRKYYDSRHCVTNSTCNQAIMLVTDGVAGNTTEVFQKYNWG 370

Qy        357 ------PDCKVRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLS 410
                   ||||||:|:||:    ::|:|| |:|||: : || :  | |::|: |::
Db        371 NGENGTSQMDTRVFTYLLGKEVTKVREIQWMACLNRGYYSHVQTLDEVHEEVLKYVDVIA 430

Qy        411 RPMVI-NHDHDIIWTEAYMDSKL--LSSQAQSLTLLTTVAMPVFSK----KNETRSHGIL 463
               |:|: |  |   || |: |      :|  :   |: :| :| | :     | |     |
Db        431 TPLVLQNEQHPPTWTHAFTDKTYDPKTSNEKRPRLMISVGVPAFDRFYRHANSTNPRARL 490

Qy        464 LGVVGSDVALRELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYN 523
               ||| |:|| : :: ||   |||||:||:|: :||||:| ||||||:   ||     ||||
Db        491 LGVAGTDVPVEDIDKLTLPYKLGVNGYSFVVSNNGYVLLHPDLRPIGTNGKM---NPNYN 547

Qy        524 SVDLSEVE--WEDQA-----ES---LRTAMINRETGTL-SMDVKVPMDKGKRVLFLTNDY 572
               |:| :|||  :|||:     ||   :| ||:  |     |: ||   || :||     ||
Db        548 SIDFTEVEHLFEDQSPREPGESILHIRNAMVRHEANEFKSISVKFHYDKMRRVSEEKQDY 607

Qy        573 FFTDISDTPFSLGAVLSRGHGE-YILLG-----NTSVEEGLHDL-------LHPDLALAG 619
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Db        608 FFAPLPNTPFTLGIVMPSEYGKTWIKVGEEVDKNKHMKINISDFFIGENWKVHP------ 661

Qy        620 DWIYCITDIDPDHRKLSQLEAMIR-FLTRKDPDLE------------------------- 653
               ||:||        | :    || :| || :   | :
Db        662 DWVYCKYHYLEGH-EFKTPEAELREFLAKMQNDWKWSEQYAEDESDWDDKDDLNCGRKTL 720

Qy        654 ------CDEELVREVLFDAVVTAPMEAYWTALALNMSEESEHV----VDMAFLGTRAGLL 703
                   |::|||  ::||| ||       |        || : :     |: |: | :||
Db        721 GDDAYYCNKELVNLLIFDAKVTNSSYGVW---RFESDEERQLIERFRADLRFVATMSGLT 777

Qy        704 RSSLFVGSEKV-SDRKF----LTPEDEASVFTLDRFPLWYRQA----SEHPAGSFVFNLR 754
               |    |  :| :||:|    |  ||          ||: |     |  | |||::::
Db        778 RWQFIFGEVEVDTDREFGDYHTTAIDET----------WYKSAILQHHEDRAESFVYSVK 827

Qy        755 WAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVD-- 812
               : : |    | : |||| |:       : | |   | |     |   : |       : ||
Db        828 YYDDPMEDSE-VKVTASHAIFPRDGGKEAPACVVGFQ----FSHARMWERFFNITAVDHC 882

Qy        813 GPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYD 872
                 | | |:|| ||||| :|:| :    ||:| ||  | |:|  ::  |:|  : :||
Db        883 NHCLPICTDDDVDCVVIDNNAYIVIGQNINTTGKFFGEFHGDVMTAMVERGIFLSIEVYD 942

Qy        873 YQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFL--LEWSVWGSWY-------- 922
               ||  ||       |   |: |:       ::|:  |       ::|   |: :
Db        943 YQEQCKEEPKAGSDGHGLLHPLRLLSLGWKYLVGRLFFEYQRIQWWADGAPFMEYTDEIE 1002

Qy        923 -----------------DRGAEAKSVFHHSHKHKKQDPL-QPCDTEYPVFVYQP-AIRE 962
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Db       1003 DEYVAVGDGGKSSASKPKDDSDDENAMF----DEPEPDPIYKACDKRSTLYALQPSALVG 1058

Qy        963 ANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPP-----VLQEATEVKYNASVK 1017
               |  ||  |  : |:|::|||||:|:|       ::  |     :   |   ::|:
Db       1059 INDFVE-APSTRPFLVKKIPNSNLVLVVV------NVLMPSRSVRLTTEPQRMEYDKEFP 1111

Qy       1018 CDRMR-SQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCP 1063
              | ::  |   ||| : |:  | :  :     : | :|   | | | |  .
Db       1112 CYKLNMSFYERRRIEECYTVHEDEELYT---YCGNASRLVLTLQLMP 1155


RESULT 11
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ID   Q9VJM0      PRELIMINARY;      PRT;  2190 AA.
AC   Q9VJM0; Q9NK64;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   CG12455-PA (Hypothetical protein BG:DS07473.1).
GN   Name=BG:DS07473.1; ORFNames=CG12455;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
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RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkul'ov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE003650; AAF53505.2; -.
DR EMBL; AE003415; AAF44988.1; -.
DR FlyBase; FBgn0028859; CG12455.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Hypothetical protein.
SQ SEQUENCE 2190 AA; 249754 MW; B8C657A2F80F226E CRC64;

Query Match 25.2%; Score 1441; DB 2; Length 2190;
Best Local Similarity 32.3%; Pred. No. 3.7e-78;
Matches 378; Conservative 187; Mismatches 373; Indels 234; Gaps 44;

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Qy        16 WADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRRKVE 75
             ||  || :|:    | : |  :::|||  | : ::|  :| ||::  ::::  || ||:: 
Db        20 WATQFGDELFALAQKITKSQEIKEKYK--EYNARVELKNGTELIKSITKNVGRMLARKMD 77

Qy        76 AVQNLVEAAEEADLNHEFNESLV---FDYYNSVLI----NERDE----KGNFVELGAEFL 124
             ||: : | ||  : | ||| :     | |::|       |  :|    :  |  :
Db        78 AVRCIQERAEYVNENFEFNLTYALQNFTYFSSKYSTFNGNSSEELEPNEAEFAWMYRNME 137

Qy       125 LESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQY 184
             |  : || | ||:|  ||| :|:|:::::   :|  :  || |: || :|:| || |:|||
Db       138 LNPDTHFYNTPVDTEHSSVHVPSNIWDRSERVLKTIMWSEHLDEVFRQNYQSDPALSWQY 197

Qy       185 FGSATGFFRIYPGIKWT---PDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGL 241
             ||| ||  | ||  :||   |: :   |:||| | |||: ||  |||||:| |||| |
Db       198 FGSDTGILRHYPAAQWTDTRPNRDDADTYDCRKRSWYIETATCSKDIVILLDHSGSMTGF 257

Qy       242 RMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEEL 301
             |  :|| || :|||   |||  |: |:  |: | ||| | ||||  :| | |   :|:|
Db       258 RHHVAKFTIRSILDTFSNNDFFTILRYSSEVNDIIPCFNGALVQATPENIEVFNQQIEQL 317
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Qy        302 -MVKGVGVVDQALREAFQILKQFQEAKQ---GSLCNQAIMLISDGAVEDYEPVFEKYNW- 356
Db        318 DDPEGYANLTLAYETAFQLLRKYYDSRHCVTNSTCNQAIMLVTDGVAGNTTEVFQKYNWG 377

Qy        357 ------PDCKVRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLS 410
Db        378 NGENGTSQMDTRVFTYLLGKEVTKVREIQWMACLNRGYYSHVQTLDEVHEEVLKYVDVIA 437

Qy        411 RPMVI-NHDHDIIWTEAYMDSKL--LSSQAQSLTLLTTVAMPVFSK----KNETRSHGIL 463
Db        438 TPLVLQNEQHPPTWTHAFTDKTYDPKTSNEKRPRLMISVGVPAFDRFYRHANSTNPRARL 497

Qy        464 LGVVGSDVALRELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYN 523
Db        498 LGVAGTDVPVEDIDKLTLPYKLGVNGYSFVVSNNGYVLLHPDLRPIGTNGKM---NPNYN 554

Qy        524 SVDLSEVE--WEDQA-----ES---LRTAMINRETGTL-SMDVKVPMDKGKRVLFLTNDY 572
Db        555 SIDFTEVEHLFEDQSPREPGESILHIRNAMVRHEANEFKSISVKFHYDKMRRVSEEKQDY 614

Qy        573 FFTDISDTPFSLGAVLSRGHGE-YILLG-----NTSVEEGLHDL-------LHPDLALAG 619
Db        615 FFAPLPNTPFTLGIVMPSEYGKTWIKVGEEVDKNKHMKINISDFFIGENWKVHP------ 668

Qy        620 DWIYCITDIDPDHRKLSQLEAMIR-FLTRKDPDLE------------------------- 653
Db        669 DWVYCKYHYLEGH-EFKTPEAELREPLAKMQNDWKWSEQYAEDESDWDDKDDLNCGRKTL 727

Qy        654 ------CDEELVREVLFDAVVTAPMEAYWTALALNMSEESEHV----VDMAFLGTRAGLL 703
Db        728 GDDAYYCNKELVNLLIFDAKVTNSSYGVW---RFESDEERQLIERFRADLRFVATMSGLT 784

Qy        704 RSSLFVGSEKV-SDRKF----LTPEDEASVFTLDRFPLWYRQA----SEHPAGSFVFNLR 754
Db        785 RWQFIFGEVEVDTDREFGDYHTTAIDET----------WYKSAILQHHEDRAESFVYSVK 834

Qy        755 WAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGP 814
Db        835 YYDDPMEDSE-----------------------------------VKCNHCLPI--- 853

Qy        815 YTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQ 874
Db        854 ----CTDDDVDCVVIDNNAYIVIGQNINTTGKFFGEFHGDVMTAMVERGIFLSIEVYDYQ 909

Qy        875 AMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHH 934
Db        910 EQCK--------EEP-----KAVMEYTDEIEDEYVAV------------GDGGKS---S 940

Qy        935 SHKHK-------------KQDPL-QPCDTEYPVFVYQP-AIREANGIVECGPCQKVFVVQ 979
Db        941 ASKPKDDSDDENAMFDEPEPDPIYKACDKRSTLYALQPSALVGINDFVE-APSTRPFLVK 999

Qy        980 QIPNSNLLLLVTDPTCDCSIFPP-----VLQEATEVKYNASVKCDRMR-SQKLRRRPDSC 1033
Db       1000 KIPNSNLVLVVV------NVLMPSRSVRLTTEPQRMEYDKEFPCYKLNMSFYERRRIEEC 1053

Qy       1034 HAFHPEVRVEADRGWA-----GFSSPNPLCLG 1060
Db       1054 YTVHEDLS-DIDTGNAHKQHNKDSFPNPYSNG 1084
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RESULT 12
Q7Q758
ID Q7Q758 PRELIMINARY; PRT; 1028 AA.
AC Q7Q758;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP5954 (Fragment).
GN Name=agCG56326; ORFNames=ENSANGG00000018729;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC   EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC   preliminary data.
DR EMBL; AAAB01008960; EAA10906.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
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FT NON_TER   1028   1028
SQ SEQUENCE   1028 AA; 118517 MW; 5A6E0DA689ABCFF9 CRC64;

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  Matches 349; Conservative 181; Mismatches 333; Indels 191; Gaps   29;

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Qy         13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEV---DGLELVRKFSEDMENM 69
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Qy         70 LRRKVEAVQNLVEAAEEADLNHEFNESLV---FDYYNSVLINERDEKGNFVEL------- 119
Db         57 MDAKVSAVKRIMDTAENTAIS--FDEEPVNQSFQYYNA---KQMIEPGEIITTPIPMIDE 111

Qy        120 ----------GAEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAV 169
Db        112 DPADITTPIPPKEIVLTKKRHFFNEAVNTTVSSVHVPTNVYDRATEVIKAIKWSEALDSI 171

Qy        170 FVENFQRDPTLTWQYFGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIV 229
Db        172 FYNNYIGDPTLTWQYFGSSSGFLRQFPATKW--EQDPVDLYDCRLRSWYIEAANSPKDML 229

Qy        230 ILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRD 289
Db        230 ILVDSSGSMTGQRKDIAKHVVSNILDTLGPNDYVNIFTFSEEVAEVVPCFRDTLVQANMG 289

Qy        290 NREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEP 349
Db        290 NIRELKLGMDNIETNEIANVSAALTRAFELLEQFRETRNGARCNQAIMLVSDGVPYSFDE 349

Qy        350 VFEKYNW---PDCKVRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYL 406
Db        350 VFEQFNWKELPPIPVRVFTYLIGREVADVKEIKEMACRNQGYYVHLSTMAEVREEVLNYI 409

Qy        407 HVLSRPMVIN-HDHDIIWTEAYMD---------------------------SKLL---- 433
Db        410 PVIARPLVLNKREHPVVWSEIYADVEDPKMTDWLWEIKERAEQKERFIDYRKNRVLFYSP 469

Qy        434 ----------------SSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALREL 476
Db        470 EEQHRRMIMKQRMNQDPYSNTQKYNFMTTVSVPVFDRRENATRVANILGVAGADVPIAEI 529

Qy        477 MKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWED-- 534
Db        530 KKYLKPHLLGVNGYAFIVTNNGYILTHPDFRPVFQD----ILKPAYNTVDMIEVELTDDD 585

Qy        535 --------QAESLRTAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGA 586
Db        586 QGPREFNNQLLNMRESIINQSTGAKWIRVKYHFDEMKRVSRTKRQYYWTPIKNTPFTLVV 645

Qy        587 VLSRGHGEYILLGNTSVEEGLHDL-----------------LHPDLALAGDWIYC----- 624
Db        646 TYPETYGLNRLQIRT--EDEIHRIHAKGSNVASFFTGNNWKIHP------DWVYCKYLNE 697
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Qy        625 ---ITDIDPDHRKLSQLEAM----IRFLTRKDPD-----LECDEELVREVLFDAVVTAPM 672
Db        698 HPNETFATPELELKHFLERMKLGGWKWPSNRTPPPPEHAMFCDRGLMQALVYDAKVTEWF 757

Qy        673 EAYWTALALNMSEESEHV-----VDMAFLGTRAGLLRSSLF---VGSEKVSDRKFLTPED 724
Db        758 SKNVSGSGGNKDEKGNEFKQRFGITVSFLATHSGLTRWQEYATGADESKQAEPDFSETHN 817

Qy        725 EASVFTLDRFPLWYRQASE------------------HPAGSFVFNLRWAEGPESAG-- 763
Db        818 RA----IDE--VWYKRAVELYYSNRNRKGADGENGKDDSDRNSFVYSV-----PFDAGNR 866

Qy        764 EPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSD 823
Db        867 NDTLVTASHAIFHADGAREAPVAVVGFQFHHSALYTLFKNITSQCGHGDPRCEKTCFTGD 926

Qy        824 LDCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHH 883
Db        927 YQCYVIDNNGFVVISEQLQETGAFFGEVKPAFMQRLLDDSIFRNVTVYDYQAVCFMAKGS 986

Qy        884 HSAAQPLVSPISAFLTATRWLLQELVLFLLEWSV 917
Db        987 INLGTVLQTP----LRLLWWLLTNTFSYLV-WVV 1015


RESULT 13
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ID   Q7PM00      PRELIMINARY;      PRT;  1011 AA.
AC   Q7PM00;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000020925 (Fragment).
GN   Name=ENSANGG00000018436;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008980; EAA14572.2; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 1.
DR   Pfam; PF00092; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
FT   NON_TER    1011   1011
SQ   SEQUENCE   1011 AA;  117662 MW;  70C7D6B71CC93E59 CRC64;

  Query Match             24.4%;  Score 1398;  DB 2;  Length 1011;
  Best Local Similarity   33.2%;  Pred. No. 4.8e-76;
  Matches  340;  Conservative  184;  Mismatches  351;  Indels  150;  Gaps   32;

Qy         16 WADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLRRKVE 75
Db          4 WADNFGEELWDLAQTMTKAMEITAKYKAYNA--RVEHKDGTALIQSIVENVGRMFIRKMD 61

Qy         76 AVQNLVEAAEEADLNHEFNESLV--FDYYNSVLIN-----ERDEKGNFVE---LGAEFLL 125
Db         62 AIKCIINLAEELSEQFEFNETLADNFSYYSSKYSNIDGRPEPEIPETLQENMWMYRNMSL 121

Qy        126 ESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYF 185
Db        122 NPDTHFFNISVNTSYSSVHVPQNVYDRYPWVLEALQWSESLDDVFLQNYNSDPALSWQYF 181

Qy        186 GSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTI 245
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Db        182 GSYTGMLRHYPALEWNREH--VDTFDCRKRSWYIETATCSKDIVILLDNSGSMTGYRNYI 239

Qy        246 AKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFK----------------------GI 282
Db        240 AQLTVKSILDTFSNNDFINIYKYSNDVEPLVPCFKVGLKILDEKCNERVRFNNTSLLQDM 299

Qy        283 LVQADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQ----GSLCNQAIML 338
Db        300 LVQATPENMRFFNEYVRELLPEGYANVKKAFVAAFELLQKYREIRRCNESVSGCNQAIML 359

Qy        339 ISDGAVEDYEPVFEKYNW----PDCKVRVFTYLIGREVSFADRMKWIACNNKGYYTQIST 394
Db        360 ITDGVPSNITEVFEAYNWFENGTKIPVRVFTYLLGREVTKVREIQWMACLNRGYYSHIQS 419

Qy        395 LADTQENVMEYLHVLSRPMVINH-DHDIIWTEAYMDS--KLL--SSQAQSLTLLTTVAMP 449
Db        420 LDEVQEEVLKYVTVIATPLVLQGVEHPPTWTHAFTDTAENLLTEADDDEPPRLMIAVGAP 479

Qy        450 VFSKK----NETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAFLNTNNGYILSHPD 505
Db        480 AFDRKANHYNETRT-ARLLGVAGTDIPVEDLDELTLPYKLGVNGYSFIVSNNGYVLMHPD 538

Qy        506 LRPLYREGKKLKPKPNYNSVDLSEVEW----------EDQAE--------SLRTAMINRE 547
Db        539 LRPV----SNGRLKENYNSIDLTEIEQIYDENITRQIEDMTGREMSPFILELRQHLVDSQ 594

Qy        548 TGTLS-MDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGE-YILLG-----N 600
Db        595 FGNMTKLPVRFHYDKMRRVSLEYQDYYYAPLENTPFSLGLVLPHDYGSTWIKVGDEIKRN 654

Qy        601 TSVEEGLHDL-------LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTR------ 647
Db        655 QHMGLNISDFFMGDNWKVHP------DWVYCKYHYLEGHEFKTPEDELRHFLNRLYEPTW 708

Qy        648 -------------------------KDPDLECDEELVREVLFDAVVTAPMEAYWTALALN 682
Db        709 KWSQQYEPEPNEKESDGPNCGRKTLDDDAYYCNKELVQLLIFDAKVTNNSYRNWEF---- 764

Qy        683 MSEESEHVVDM-----AFLGTRAGLLRSSLFVGSEKV-SDRKFLTPEDEASVFTLDRFPL 736
Db        765 ENENERKIIEMYNATLRFVATMSGLTRWQFIFGEVEVDTDSEFGDYHKKA----IDE--T 818

Qy        737 WYRQA-SEHPAG--SFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMK 793
Db        819 WYRSAILQHKIDPKSFVYSVPHESDPPEDGE-LKVTATMAIFPRDGGLEAPGCVTGFQFT 877

Qy        794 LEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEVDG 853
Db        878 HSLMYDRFMEITSK-TTCDG-CIETCASESRDCYVIDHNGYVVLSETSNHTGRFFGEIEG 935

Qy        854 AVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFLL 913
Db        936 AIMQSMVDKEIFTMITVFDLQGLCEYERVVENDAIALLHPMKVFMLGLKWLIAEIAIMLS 995

Qy        914 EWSVW 918
Db        996 RFDFW 1000


RESULT 14
Q9NK83
ID   Q9NK83      PRELIMINARY;      PRT;  1255 AA.
AC   Q9NK83;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein BG:DS07108.2.
GN   Name=BG:DS07108.2; ORFNames=CG4587;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
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OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=99403001; PubMed=10471707;
RA   Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA   Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA   Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA   Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA   Celniker S., Rubin G.M.;
RT   "An exploration of the sequence of a 2.9-Mb region of the genome of
RT   Drosophila melanogaster: the Adh region.";
RL   Genetics 153:179-219(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA   Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA   Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA   Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA   Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA   Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA   Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA   Zieran L.L., Rubin G.M.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003413; AAF44957.1; -.
DR   FlyBase; FBgn0028863; CG4587.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 1.
DR   Pfam; PF00092; VWA; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   1255 AA;  140745 MW;  FEB584D76C7785C6 CRC64;

  Query Match           22.8%;  Score 1305.5;  DB 2;  Length 1255;
  Best Local Similarity  29.1%;  Pred. No. 2.8e-70;
  Matches  328;  Conservative  203;  Mismatches  403;  Indels  195;  Gaps   30;

Qy        80 LVEAAEEADLNHEFNESLV------FDYYNSVLINERDEKGNFVELGAEFLLESNAHFSN 133
             |:::||:| |:    :          :|::  ||| :  |   :      :      |
Db       116 LMDSAEQAALSELEGQGQAESPMGGQQHYDARRINEYNADGKLADGARHMDIRFMRRFER 175

Qy       134 LPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFFR 193
             |||| |:||: :|  |   :||: : :  |  |: :|  | ::|| |:||||||:||| |
Db       176 LPVNLSLSSILVPHGVDLDEPDVKSALQWSGHLDPLFQNNLEQDPALSWQYFGSSTGFLR 235

Qy       194 IYPGIKWTPD--ENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTIT 251
              :||  | |:  :   :  | |   |::|||:|||||:||:| | ||      :  |
Db       236 RFPGTAWPPEGSKGSKLIHDFRTHNWFVQAASSPKDIMILLDASSSMTEKSFDLGMATAF 295

Qy       252 TILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQ 311
             |||||||:||||:| ::: |    ||||  :|:|  || :  |  |: : ::
Db       296 NILDTLGEDDFVNLITFSEVVKTPVPCFKDRMVRATPDNIQEIKSAVKAIKLQDTANFTA 355

Qy       312 ALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGRE 371
             |  || :| :: ::  || ||||||||::   | :: | ::|||   ||:|||||| :
Db       356 GLEYAFSLLHKYNQSGAGSQCNQAIMLITESTSESHKDVIKQYNWPHMPVRIFTYLIGSD 415

Qy       372 VSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVI-NHDHDIIWTEAYMDS 430
                  :  :||:|||:: ||:   : :  |::|  |::|||::   || : |:  ::
Db       416 SGSRSNLHDMACSNKGFFVQINDYDEARRKVIDYALVMARPMIMYQADHPVHWSPVFVAG 475

Qy       431 K---LLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGV 487
             |   |          |:|||: ||| ::| :      ||||||:|| : |: |: |::|||
Db       476 KSGGLGRDSEYQRRLVTTVSTPVFDRRNHSVRVANLLGVVGTDVPIEEIRKVIPQHKLGP 535

Qy       488 HGYAFLNTNNGYILSHPDLRPLYREGKKL-KPKPNYNSVDLSEVEW------------- 532
             :||:|:  ||| :| |||||||    : : : || | |||::|:|
Db       536 NGYSFIVDNNGRVLYHPDLRPLGDANQYIDQLKPKYASVDITELELPETEFGNNNEPIEI 595

Qy       533 -EDQAESLRTAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRG 591
              ::    :| ||  : |     |   |  |||   |: ||:  | ||||:|  ||
Db       596 NKNLLNEMRGDMIKPKEGETEFTVMNHYDDSKRVSTRTHRYFYGPIEDTPFTLAIVLPEK 655

Qy       592 HGEYILLGNTSVEEGLHDL----------LHPDLALAGDWIYC----ITDIDPDHRKLSQ 637
             :| :  :    :    :::          :||      ||:||    ::|:: :     :
Db       656 YGSHEFVSQQEIRHSRNNVTEYFKGDNWRVHP------DWVYCEYNSVSDLEKERESSGE 709

Qy       638 L------------EAMIRFL--------------------------------TRKDPDLE 653
                         |  :|                                    :||
Db       710 YSSRDQEPSFGSPEEQVRPKSPQPHHNMHSGSNGGNAPGSSHFGSQHQSSQGSRKAEPYF 769

Qy       654 CDEELVREVLFDAVVTAPMEAYWTALALNMSEESE----HVVDMAFLGTRAGLLRSSLFV 709
             ||  |:: :: ||:||  ::   |  :    :: :      ||  :|: ||:|||   ::
Db       770 CDRALLQSLVRDAMVTDGLDRNTTGSSSGKEDKQQGYQKFVVATSFVATRSGLLR---WI 826

Qy       710 GSEKVSDRKFLTPE---DEASVFTLDRFPLWYRQA-SEHPA--GSFVFNLRWAEGPESAG 763
                |   |  |||    | :|  :|    ||::|  :|     |||::: :  |
Db       827 DHVK---RPEDTPEPHFSEDNVRAMD--TSWYKRAIDQHSVEPDSFVYSVPFGSGYAIKS 881

Qy       764 EPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSD 823
               :|||| |: |      | |   |:| : : | : |   |  |: : |   ::|   :
Db       882 NATLVTASHAIFVEHRGHKAAAGVVGLQFQHDSLAKHFINITSACTGMTG-CKRTCASDN 940

Qy       824 LDCFVIDNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHH 883
             |||:|:||:||::||:    ||:| |::|| ::  |:   :: :||: ||| :|  : : :
Db       941 LDCYVLDNSGFVIISEEMEHTGKFFGQIDGTIMDSLVQDRIYKRVTVNDYQGVCSDADNP 1000

Qy       884 HSAAQPLVSPISAFLTATRWLLQELVLFLLEW--------------------------S 916
             ::||  :: |          |    |:     |                         :
Db      1001 YTAAGGILKP----NRLGSWFFNHLLALSAAWLSLMPASLRAWPQEEYTYDNEDVVFVDN 1056

Qy       917 VWGSWYDRG------------------AEAKSVFHHSHKHK-------KQDP--LQPCD 948
               :  |: |                |: :       :||          ||   : ||
Db      1057 NYSDEYEFGNENEYNMQVDQEMDEFFTTADVEYTTPPPRQHKPHVGPRFSPDPHNARRCD 1116

Qy       949 TEYPVFVYQPAIREANG--------IVEC--GPCQKVFVVQQIPNSNLLLLVTDPTCDC- 997
             :::  ||       |        :  |    |:: | ||:||:|||:|||  |  | |
Db      1117 LRTDLYMLQPERLNQGGQNNPLKGKLTNCHVSGCERPFSVQKIPHSNLILLVVDTLCPCG 1176

Qy       998 ----SIFPPVLQEATEVKYNASVKCDRMR---SQKLRRRPDSCHAFHPE 1039
                  | |  |:||  :       |   |    |: ||||  |  :|||
Db      1177 SKQLDIEP--LEEAGVIG-----ACSTRRQGQEQESRRRPKKCINYHPE 1218


RESULT 15
Q9VJN7
ID   Q9VJN7      PRELIMINARY;      PRT;  1120 AA.
AC   Q9VJN7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CG4587-PA.
GN   ORFNames=CG4587;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
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RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003648; AAF53476.2; -.
DR   FlyBase; FBgn0028863; CG4587.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR004010; Cache.
DR   InterPro; IPR002035; VWF_A.
DR   Pfam; PF02743; Cache; 1.
DR   Pfam; PF00092; VWA; 1.
DR   SMART; SM00327; VWA; 1.
DR   PROSITE; PS50234; VWFA; 1.
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  Best Local Similarity   28.9%;  Pred. No. 5.5e-69;
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Db        27 HYDARRINEYNADGKLADGARHMDIRFMRRFERLPVNLSLSSILVPHGVDLDEPDVKSAL 86

Qy       161 YMSEALNAVFVENFQRDPTLTWQYFGSATGFFRIYPGIKWTPD--ENGVITFDCRNRGWY 218
Db        87 QWSGHLDPLFQNNLEQDPALSWQYFGSSTGFLRRFPGTAWPPEGSKGSKLIHDFRTHNWF 146

Qy       219 IQAATSPKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPC 278
Db       147 VQAASSPKDIMILLDASSSMTEKSFDLGMATAFNILDTLGEDDFVNLITFSEVVKTPVPC 206

Qy       279 FKGILVQADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIML 338
Db       207 FKDRMVRATPDNIQEIKSAVKAIKLQDTANFTAGLEYAFSLLHKYNQSGAGSQCNQAIML 266

Qy       339 ISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADT 398
Db       267 ITESTSESHKDVIKQYNWPHMPVRIFTYLIGSDSGSRSNLHDMACSNKGFFVQINDYDEA 326

Qy       399 QENVMEYLHVLSRPMVI-NHDHDIIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNET 457
Db       327 RRKVIDYALVMARPMIMYQADHPVHWSPVFV----------------AVSTPVFDRRNHS 370

Qy       458 RSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKL- 516
Db       371 VRVANLLGVVGTDVPIEEIRKVIPQHKLGPNGYSFIVDNNGRVLYHPDLRPLGDANQYID 430

Qy       517 KPKPNYNSVDLSEVEW---------------EDQAESLRTAMINRETGTLSMDVKVPMDK 561
Db       431 QLKPKYASVDITELELPETEFGNNNEPIEINKNLLNEMRGDMIKPKEGETEFTVMNHYDD 490

Qy       562 GKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL----------L 611
Db       491 SKRVSTRTHRYFYGPIEDTPFTLAIVLPEKYGSHEFVSQQEIRHSRNNVTEYFKGDNWRV 550

Qy       612 HPDLALAGDWIYC----ITDIDPDHRKLSQL-----------EAMIRFL---------- 645
Db       551 HP------DWVYCEYNSVSDLEKERESSGEYSSRDQEPSFGSPEEQVRPKSPQPHHNMHS 604

Qy       646 ----------------------TRKDPDLECDEELVREVLFDAVVTAPMEAYWTALALNM 683
Db       605 GSNGGNAPGSSHFGSQHQSSQGSRKAEPYFCDRALLQSLVRDAMVTDGLDRNTTGSSSGK 664

Qy       684 SEESE----HVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPE---DEASVFTLDRFPL 736
Db       665 EDKQQGYQKFVVATSFVATRSGLLR---WIDHVK---RPEDTPEPHFSEDNVRAMD--TS 716

Qy       737 WYRQA-SEHPA--GSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMK 793
Db       717 WYKRAIDQHSVEPDSFVYSVPFGSGYAIKSNATLVTASHAIFVEHRGHKAAAGVVGLQFQ 776

Qy       794 LEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEVDG 853
Db       777 HDSLAKHFINITSACTGMTG-CKRTCASDNLDCYVLDNSGFVIISEEMEHTGKFFGQIDG 835

Qy       854 AVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFLL 913
Db       836 TIMDSLVQDRIYKRVTVNDYQGVCSDADNPYTAAGGILKP----NRLGSWFFNHLLALSA 891

Qy       914 EW--------------------------SVWGSWYDRG------------------AE 927
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Qy        928 AKSVFHHSHKHK-------KQDP--LQPCDTEYPVFVYQPAIREANG--------IVEC- 969
                :         :||          ||    : ||     ::: ||       |         :   |
Db        952 VEYTTPPPRQHKPHVGPRFSPDPHNARRCDLRTDLYMLQPERLNQGGQNNPLKGKLTNCH 1011

Qy        970 -GPCQKVFVVQQIPNSNLLLLVTDPTCDC-----SIFPPVLQEATEVKYNASVKCDRMR- 1022
                 |:: | ||:||:|||:||| |   | |       | |  |:||  :        |    |
Db       1012 VSGCERPFSVQKIPHSNLILLVVDTLCPCGSKQLDIEP--LEEAGVIG-----ACSTRRQ 1064

Qy       1023 --SQKLRRRPDSCHAFHPE 1039
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Db       1065 GQEQESRRRPKKCINYHPE 1083
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Search completed: November 16, 2005, 03:22:51
Job time : 196 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2005, 19:23:23 ; Search time 1314 Seconds
(without alignments)
4910.592 Million cell updates/sec

Title: US-09-833-222A-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTPVPVLLGGNIRVYAL 1090

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_h/US09833222/runat_15112005_145357_15779/app_query.fasta_1.1287
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5726	100.0	3486	10	ADF71819	Adf71819 Human cal
2	5726	100.0	3486	10	ABZ20598	Abz20598 Human vol
3	5386.5	94.1	5073	3	AAA09254	Aaa09254 Human alp
4	5385.5	94.1	4841	10	ADE07110	Ade07110 Novel cod
5	5342.5	93.3	3339	4	AAS01433	Aas01433 Human sec
6	5342.5	93.3	3339	5	AAF57570	Aaf57570 Human cal
7	5276	92.1	3209	4	AAS01432	Aas01432 Human sec
8	5276	92.1	3209	5	AAF57569	Aaf57569 Human cal
9	5234.5	91.4	3228	6	AAS17581	Aas17581 DNA encod
10	5230.5	91.3	3345	6	AAS17582	Aas17582 DNA encod
11	5197.5	90.8	5713	3	AAA09278	Aaa09278 Human alp
12	5148	89.9	3201	4	AAS01431	Aas01431 Human sec
13	5148	89.9	3201	5	AAF57568	Aaf57568 Human cal
14	5127.5	89.5	3742	13	ADN33188	Adn33188 Human tra
15	3808	66.5	4125	6	AAD22004	Aad22004 Human tra
16	3416.5	59.7	3690	6	AAD26399	Aad26399 Human cal
17	3410.5	59.6	3770	3	AAA09253	Aaa09253 Human alp
18	3410.5	59.6	3770	4	AAS01414	Aas01414 Human sec
19	3410.5	59.6	3770	5	AAF57551	Aaf57551 Human cal
20	3400.5	59.4	3213	4	AAS01409	Aas01409 Human sec
21	3400.5	59.4	3213	5	AAF57546	Aaf57546 Human cal
22	3326.5	58.1	3114	4	AAS01408	Aas01408 Human sec
23	3326.5	58.1	3114	5	AAF57545	Aaf57545 Human cal
24	3278.5	57.3	3057	4	AAS01407	Aas01407 Human sec
25	3278.5	57.3	3057	5	AAF57544	Aaf57544 Human cal
26	3222	56.3	3598	3	AAA09261	Aaa09261 Human alp
27	3195.5	55.8	3382	8	ABZ23112	Abz23112 Nucleotid
28	2306	40.3	1523	10	ADK41000	Adk41000 Novel hum
29	2306	40.3	1523	13	ADR15714	Adr15714 Kinase 41
30	2218	38.7	1452	3	AAA09279	Aaa09279 Human alp
31	2026.5	35.4	2008	3	AAA09260	Aaa09260 Human alp
32	1959.5	34.2	1774	3	AAZ51626	Aaz51626 Human mem
33	1792.5	31.3	1050	4	AAS01412	Aas01412 Human sec
34	1792.5	31.3	1050	5	AAF57549	Aaf57549 Human cal
35	1695	29.6	969	4	AAS01411	Aas01411 Human sec
36	1695	29.6	969	5	AAF57548	Aaf57548 Human cal
37	1598	27.9	912	4	AAS01410	Aas01410 Human sec
38	1598	27.9	912	5	AAF57547	Aaf57547 Human cal
39	1565	27.3	4892	12	ADO16904	Ado16904 Tobacco b
40	1554.5	27.1	5028	12	ADO16902	Ado16902 Tobacco b
41	1497.5	26.2	5862	5	AAD05208	Aad05208 D. melano
42	1410	24.6	6519	4	ABL22283	Abl22283 Drosophil
43	1392.5	24.3	4383	12	ADO16900	Ado16900 Tobacco b
44	1362.5	23.8	856	4	AAS31088	Aas31088 Human dia
45	1336.5	23.3	3414	4	ABL10835	Abl10835 Drosophil

ALIGNMENTS

RESULT 1
ADF71819
ID ADF71819 standard; cDNA; 3486 BP.
XX
AC ADF71819;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human calcium channel alpha2delta4 subunit cDNA.
XX
KW neuroprotective; cytostatic; gene therapy; calcium channel;
KW alpha2delta-4; amyotrophic lateral sclerosis; multiple sclerosis; cancer;
KW human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 190. .3462
FT /*tag= a
FT /product= "Human calcium channel alpha2delta4 subunit"
XX
PN US2003170785-A1.
XX
PD 11-SEP-2003.
XX
PF 10-APR-2002; 2002US-00119624.
XX
PR 11-APR-2001; 2001US-00833222.
XX

PA (QINN/) QIN N.
PA (CODD/) CODD E.
XX
PI Qin N, Codd E;
XX
DR WPI; 2003-898262/82.
DR P-PSDB; ADF71820.
XX
PT New human alpha2 delta4 calcium channel subunit protein and nucleic acid
PT molecule, useful for diagnosing and treating diseases associated with
PT defective calcium channel subunit, e.g. cancer and multiple sclerosis.
XX
PS Claim 10; SEQ ID NO 9; 37pp; English.
XX
CC The invention describes a new isolated and purified nucleic acid molecule
CC comprising: a sequence having at least a 70% identity to nucleotides 1-
CC 224 or 3308-3486 of a sequence of 3486 bp (S1) fully defined in the
CC specification; at least 15 sequential bases of the polynucleotide of (a);
CC or a sequence that is complementary to the polynucleotide of (a) or (b).
CC Specifically claimed is an alpha2delta-4 nucleic acid molecule comprising
CC a sequence of 3486 bp fully defined in the specification and encoding an
CC alpha2delta-4 calcium channel subunit protein having a sequence of 1090
CC amino acids fully defined in the specification. The nucleic acid molecule
CC and polypeptide are useful in diagnosing and treating a disease or
CC disorder associated with a defective alpha2delta-4 subunit, such as
CC amyotrophic lateral sclerosis, multiple sclerosis or cancer. The methods
CC may be used for identifying compounds capable of treating the above-
CC mentioned diseases or disorders. This sequence encodes human calcium
CC channel alpha2delta-4 subunit.
XX
SQ Sequence 3486 BP; 827 A; 957 C; 1009 G; 693 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3486
Score:	5726.00	Matches:	1090
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-833-222A-10 (1-1090) x ADF71819 (1-3486)

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Qy          1 MetAlaValAlaLeuGlyThrArgArgArgAspArgValLysLeuTrpAlaAspThrPhe 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 ATGGCTGTAGCTTTAGGGACAAGGAGGAGGGACAGAGTGAAGCTATGGGCTGACACCTTC 249

Qy         21 GlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeuLeuLeuGlnLysLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GGCGGGGACCTGTATAACACTGTGACCAAATACTCAGGCTCTCTCTTGCTGCAGAAGAAG 309

Qy         41 TyrLysAspValGluSerSerLeuLysIleGluGluValAspGlyLeuGluLeuValArg 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 TACAAGGATGTGGAGTCCAGTCTGAAGATCGAGGAGGTGGATGGCTTGGAGCTGGTGAGG 369

Qy         61 LysPheSerGluAspMetGluAsnMetLeuArgArgLysValGluAlaValGlnAsnLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AAGTTCTCAGAGGACATGGAGAACATGCTGCGGAGGAAAGTCGAGGCGGTCCAGAATCTG 429

Qy         81 ValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGluSerLeuValPheAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GTGGAAGCTGCCGAGGAGGCCGACCTGAACCACGAATTCAATGAATCCCTGGTGTTCGAC 489

Qy        101 TyrTyrAsnSerValLeuIleAsnGluArgAspGluLysGlyAsnPheValGluLeuGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TATTACAACTCGGTCCTGATCAACGAGAGGGACGAGAAGGGCAACTTCGTGGAGCTGGGC 549

Qy        121 AlaGluPheLeuLeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIle 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GCCGAGTTCCTCCTGGAGTCCAATGCTCACTTCAGCAACCTGCCGGTGAACACCTCCATC 609

Qy        141 SerSerValGlnLeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyVal 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AGCAGCGTGCAGCTGCCCACCAACGTGTACAACAAAGACCCAGATATTTTAAATGGAGTC 669

Qy        161 TyrMetSerGluAlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 TACATGTCTGAAGCCTTGAATGCTGTCTTCGTGGAGAACTTCCAGAGAGACCCAACGTTG 729

Qy        181 ThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 ACCTGGCAATATTTTGGCAGTGCAACTGGATTCTTCAGGATCTATCCAGGTATAAAATGG 789

Qy        201 ThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 ACACCTGATGAGAATGGAGTCATTACTTTTGACTGCCGAAACCGCGGCTGGTACATTCAA 849

Qy        221 AlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMetLysGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 GCTGCTACTTCTCCCAAGGACATAGTGATTTTGGTGGACGTGAGCGGCAGTATGAAGGGG 909

Qy        241 LeuArgMetThrIleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAsn 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 CTGAGGATGACTATTGCCAAGCACACCATCACCACCATCTTGGACACCCTGGGGGAGAAT 969

Qy        261 AspPheValAsnIleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLys 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 GACTTCGTTAATATCATAGCGTACAATGACTACGTCCATTACATCGAGCCTTGTTTTAAA 1029

Qy        281 GlyIleLeuValGlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuValGluGlu 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GGGATCCTCGTCCAGGCGGACCGAGACAATCGAGAGCATTTCAAACTGCTGGTGGAGGAG 1089

Qy        301 LeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 TTGATGGTCAAAGGTGTGGGGGTCGTGGACCAAGCCCTGAGAGAAGCCTTCCAGATCCTG 1149

Qy        321 LysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSer 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 AAGCAGTTCCAAGAGGCCAAGCAAGGAAGCCTCTGCAACCAGGCCATCATGCTCATCAGC 1209

Qy        341 AspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLys 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 GACGGCGCCGTGGAGGACTACGAGCCGGTGTTTGAGAAGTATAACTGGCCAGACTGTAAG 1269

Qy        361 ValArgValPheThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrp 380
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Db       1270 GTCCGAGTTTTCACTTACCTCATTGGGAGAGAAGTGTCTTTTGCTGACCGCATGAAGTGG 1329

Qy        381 IleAlaCysAsnAsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGlu 400
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Db       1330 ATTGCATGCAACAACAAAGGCTACTACACGCAGATCTCAACGCTGGCGGACACCCAGGAG 1389

Qy        401 AsnValMetGluTyrLeuHisValLeuSerArgProMetValIleAsnHisAspHisAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 AACGTGATGGAATACCTGCACGTGCTCAGCCGCCCCATGGTCATCAACCACGACCACGAC 1449

Qy        421 IleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 ATCATCTGGACAGAGGCCTACATGGACAGCAAGCTCCTCAGCTCGCAGGCTCAGAGCCTG 1509

Qy        441 ThrLeuLeuThrThrValAlaMetProValPheSerLysLysAsnGluThrArgSerHis 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1510 ACACTGCTCACCACTGTGGCCATGCCAGTCTTCAGCAAGAAGAACGAAACGCGATCCCAT 1569

Qy        461 GlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GGCATTCTCCTGGGTGTGGTGGGCTCAGATGTGGCCCTGAGAGAGCTGATGAAGCTGGCG 1629

Qy        481 ProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIle 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 CCCCGGTACAAGCTTGGAGTGCACGGATACGCCTTTCTGAACACCAACAATGGCTACATC 1689

Qy        501 LeuSerHisProAspLeuArgProLeuTyrArgGluGlyLysLysLeuLysProLysPro 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 CTCTCCCATCCCGACCTCCGGCCCCTGTACAGAGAGGGGAAGAAACTAAAACCCAAACCT 1749
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Qy       521 AsnTyrAsnSerValAspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArg 540
Db      1750 AACTACAACAGTGTGGATCTCTCCGAAGTGGAGTGGGAAGACCAGGCTGAATCTCTGAGA 1809

Qy       541 ThrAlaMetIleAsnArgGluThrGlyThrLeuSerMetAspValLysValProMetAsp 560
Db      1810 ACAGCCATGATCAATAGGGAAACAGGTACTCTCTCGATGGATGTGAAGGTTCCGATGGAT 1869

Qy       561 LysGlyLysArgValLeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThr 580
Db      1870 AAAGGGAAGCGAGTTCTTTTCCTGACCAATGACTACTTCTTCACGGACATCAGCGACACC 1929

Qy       581 ProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsn 600
Db      1930 CCTTTCAGTTTGGGGGCGGTGCTGTCCCGGGGCCACGGAGAATACATCCTTCTGGGGAAC 1989

Qy       601 ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAsp 620
Db      1990 ACGTCTGTGGAAGAAGGCCTGCATGACTTGCTTCACCCAGACCTGGCCCTGGCCGGTGAC 2049

Qy       621 TrpIleTyrCysIleThrAspIleAspProAspHisArgLysLeuSerGlnLeuGluAla 640
Db      2050 TGGATCTACTGCATCACAGATATTGACCCAGACCACCGGAAGCTCAGCCAGCTAGAGGCC 2109

Qy       641 MetIleArgPheLeuThrArgLysAspProAspLeuGluCysAspGluGluLeuValArg 660
Db      2110 ATGATCCGCTTCCTCACCAGGAAGGACCCAGACCTGGAGTGTGACGAGGAGCTGGTCCGG 2169

Qy       661 GluValLeuPheAspAlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAla 680
Db      2170 GAGGTGCTGTTTGACGCGGTGGTGACAGCCCCCATGGAAGCCTACTGGACAGCGCTGGCC 2229

Qy       681 LeuAsnMetSerGluGluSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700
Db      2230 CTCAACATGTCCGAGGAGTCTGAACACGTGGTGGACATGGCCTTCCTGGGCACCCGGGCT 2289

Qy       701 GlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPheLeu 720
Db      2290 GGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGTCTCCGACAGGAAGTTCCTG 2349

Qy       721 ThrProGluAspGluAlaSerValPheThrLeuAspArgProProLeuTrpTyrArgGln 740
Db      2350 ACACCTGAGGACGAGGCCAGCGTGTTCACCCTGGACCGCTTCCCGCTGTGGTACCGCCAG 2409

Qy       741 AlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGlu 760
Db      2410 GCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCTCCGCTGGGCAGAAGGACCAGAA 2469

Qy       761 SerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLys 780
Db      2470 AGTGCGGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGTGGCGGTGACCGTGGACAAG 2529

Qy       781 ArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLys 800
Db      2530 AGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAA 2589

Qy       801 PheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGlu 820
Db      2590 TTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCCGTACACACAGAGCTGCGAG 2649

Qy       821 AspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArg 840
Db      2650 GACAGTGATCTGGACTGCTTCGTCATCGACAACAACGGGTTCATTCTGATCTCCAAGAGG 2709

Qy       841 SerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeu 860
Db      2710 TCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGCTGTCCTGACCCAGCTGCTC 2769

Qy       861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
Db      2770 AGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCAGGCCATGTGCAAACCCTCG 2829

Qy       881 SerHisHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAla 900
Db      2830 AGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACGGCG 2889

Qy       901 ThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySer 920
Db      2890 ACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGCTCC 2949

Qy       921 TrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLysLys 940
Db      2950 TGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCACTCCCACAAACACAAGAAG 3009

Qy       941 GlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAlaIle 960
Db      3010 CAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCCATC 3069

Qy       961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGlnGln 980
Db      3070 CGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAG 3129

Qy       981 IleProAsnSerAsnLeuLeuLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
Db      3130 ATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATCTTC 3189

Qy      1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
Db      3190 CCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGCCTCTGTCAAATGTGACCGG 3249

Qy      1021 MetArgSerGlnLysLeuArgArgArgProAspSerCysHisAlaPheHisProGluVal 1040
Db      3250 ATGCGCTCCCAGAAGCTCCGCCGGCGACCAGACTCCTGCCACGCCTTCCATCCAGAGGTG 3309

Qy      1041 ArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGly 1060
Db      3310 CGGGTTGAGGCGGATCGAGGGTGGGCTGGATTTTCATCCCCAAACCCTCTGTGCCTGGGT 3369

Qy      1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
Db      3370 CTGTGCCCCTGCAGACAGGAGCATATAGGGATGCCAATGAACACACCTGTGCCTGTGCTT 3429

Qy      1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
Db      3430 CTCGGGGGAAACATTCGCGTTTATGCCCTG 3459
```

RESULT 2
ABZ20598
ID ABZ20598 standard; cDNA; 3486 BP.
XX
AC ABZ20598;
XX
DT 03-MAR-2003 (first entry)
XX
DE Human voltage gated calcium channel alpha2delta-4 subunit cDNA.
XX
KW Human; voltage gated calcium channel; alpha2delta-4 subunit;
KW antiparkinsonian; tranquilizer; neuroprotective; anticonvulsant;
KW antimigraine; analgesic; cytostatic; antidepressant; antiinflammatory;
KW gene therapy; epilepsy; migraine; ataxia; vestibular defect;
KW chronic pain; neuropathic pain; Parkinson's disease; depression; cancer;
KW inflammation; seizure-related syndrome; anxiety; multiple sclerosis; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   190. .3462
FT   /*tag= a
FT   /product= "calcium channel alpha2delta-4 subunit"
XX
PN WO200283847-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011297.
XX

PR 11-APR-2001; 2001US-00833222.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Qin N, Codd E;
XX
DR WPI; 2003-093006/08.
DR P-PSDB; ABP59509.
XX
PT New nucleic acid molecule encoding human alpha2 delta4 calcium channel
PT subunit protein, useful for diagnosing and treating a disease associated
PT with defects in the subunit protein, e.g. epilepsy, migraine, ataxia or
PT chronic pain.
XX
PS Claim 1; Page 56-59; 91pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC voltage gated calcium channel alpha2delta-4 subunit. The sequences are
CC useful for diagnosing and treating a disease or disorder associated with
CC a defective alpha2delta-4 subunit, such as seizure-related syndromes,
CC epilepsy, migraine, ataxia, vestibular defects, chronic pain, neuropathic
CC pain, mood, sleep interference, anxiety, ALS, multiple sclerosis, mania,
CC Parkinson's disease, substance abuse/addiction syndromes, depression,
CC cancer, or inflammation. The present sequence is the coding sequence of
CC the invention
XX
SQ Sequence 3486 BP; 827 A; 957 C; 1009 G; 693 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3486
Score:	5726.00	Matches:	1090
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-833-222A-10 (1-1090) x ABZ20598 (1-3486)

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Qy          1 MetAlaValAlaLeuGlyThrArgArgArgAspArgValLysLeuTrpAlaAspThrPhe 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 ATGGCTGTAGCTTTAGGGACAAGGAGGAGGGACAGAGTGAAGCTATGGGCTGACACCTTC 249

Qy         21 GlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeuLeuLeuGlnLysLys 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GGCGGGGACCTGTATAACACTGTGACCAAATACTCAGGCTCTCTCTTGCTGCAGAAGAAG 309

Qy         41 TyrLysAspValGluSerSerLeuLysIleGluGluValAspGlyLeuGluLeuValArg 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 TACAAGGATGTGGAGTCCAGTCTGAAGATCGAGGAGGTGGATGGCTTGGAGCTGGTGAGG 369

Qy         61 LysPheSerGluAspMetGluAsnMetLeuArgArgLysValGluAlaValGlnAsnLeu 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AAGTTCTCAGAGGACATGGAGAACATGCTGCGGAGGAAAGTCGAGGCGGTCCAGAATCTG 429

Qy         81 ValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGluSerLeuValPheAsp 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GTGGAAGCTGCCGAGGAGGCCGACCTGAACCACGAATTCAATGAATCCCTGGTGTTCGAC 489

Qy        101 TyrTyrAsnSerValLeuIleAsnGluArgAspGluLysGlyAsnPheValGluLeuGly 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TATTACAACTCGGTCCTGATCAACGAGAGGGACGAGAAGGGCAACTTCGTGGAGCTGGGC 549

Qy        121 AlaGluPheLeuLeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIle 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GCCGAGTTCCTCCTGGAGTCCAATGCTCACTTCAGCAACCTGCCGGTGAACACCTCCATC 609

Qy        141 SerSerValGlnLeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyVal 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 AGCAGCGTGCAGCTGCCCACCAACGTGTACAACAAAGACCCAGATATTTTAAATGGAGTC 669

Qy        161 TyrMetSerGluAlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeu 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 TACATGTCTGAAGCCTTGAATGCTGTCTTCGTGGAGAACTTCCAGAGAGACCCAACGTTG 729

Qy        181 ThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrp 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 ACCTGGCAATATTTTGGCAGTGCAACTGGATTCTTCAGGATCTATCCAGGTATAAAATGG 789

Qy        201 ThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGln 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 ACACCTGATGAGAATGGAGTCATTACTTTTGACTGCCGAAACCGCGGCTGGTACATTCAA 849

Qy        221 AlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMetLysGly 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 GCTGCTACTTCTCCCAAGGACATAGTGATTTTGGTGGACGTGAGCGGCAGTATGAAGGGG 909

Qy        241 LeuArgMetThrIleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAsn 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 CTGAGGATGACTATTGCCAAGCACACCATCACCACCATCTTGGACACCCTGGGGGAGAAT 969

Qy        261 AspPheValAsnIleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLys 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 GACTTCGTTAATATCATAGCGTACAATGACTACGTCCATTACATCGAGCCTTGTTTTAAA 1029

Qy        281 GlyIleLeuValGlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuValGluGlu 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GGGATCCTCGTCCAGGCGGACCGAGACAATCGAGAGCATTTCAAACTGCTGGTGGAGGAG 1089

Qy        301 LeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeu 320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 TTGATGGTCAAAGGTGTGGGGGTCGTGGACCAAGCCCTGAGAGAAGCCTTCCAGATCCTG 1149

Qy        321 LysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSer 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 AAGCAGTTCCAAGAGGCCAAGCAAGGAAGCCTCTGCAACCAGGCCATCATGCTCATCAGC 1209

Qy        341 AspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLys 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 GACGGCGCCGTGGAGGACTACGAGCCGGTGTTTGAGAAGTATAACTGGCCAGACTGTAAG 1269

Qy        361 ValArgValPheThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrp 380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 GTCCGAGTTTTCACTTACCTCATTGGGAGAGAAGTGTCTTTTGCTGACCGCATGAAGTGG 1329

Qy        381 IleAlaCysAsnAsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGlu 400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 ATTGCATGCAACAACAAAGGCTACTACACGCAGATCTCAACGCTGGCGGACACCCAGGAG 1389

Qy        401 AsnValMetGluTyrLeuHisValLeuSerArgProMetValIleAsnHisAspHisAsp 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 AACGTGATGGAATACCTGCACGTGCTCAGCCGCCCCATGGTCATCAACCACGACCACGAC 1449

Qy        421 IleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeu 440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 ATCATCTGGACAGAGGCCTACATGGACAGCAAGCTCCTCAGCTCGCAGGCTCAGAGCCTG 1509

Qy        441 ThrLeuLeuThrThrValAlaMetProValPheSerLysLysAsnGluThrArgSerHis 460
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1510 ACACTGCTCACCACTGTGGCCATGCCAGTCTTCAGCAAGAAGAACGAAACGCGATCCCAT 1569

Qy        461 GlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAla 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GGCATTCTCCTGGGTGTGGTGGGCTCAGATGTGGCCCTGAGAGAGCTGATGAAGCTGGCG 1629

Qy        481 ProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIle 500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 CCCCGGTACAAGCTTGGAGTGCACGGATACGCCTTTCTGAACACCAACAATGGCTACATC 1689

Qy        501 LeuSerHisProAspLeuArgProLeuTyrArgGluGlyLysLysLeuLysProLysPro 520
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 CTCTCCCATCCCGACCTCCGGCCCCTGTACAGAGAGGGGAAGAAACTAAAACCCAAACCT 1749

Qy        521 AsnTyrAsnSerValAspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArg 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1750 AACTACAACAGTGTGGATCTCTCCGAAGTGGAGTGGGAAGACCAGGCTGAATCTCTGAGA 1809
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Qy       541 ThrAlaMetIleAsnArgGluThrGlyThrLeuSerMetAspValLysValProMetAsp 560
Db      1810 ACAGCCATGATCAATAGGGAAACAGGTACTCTCTCGATGGATGTGAAGGTTCCGATGGAT 1869

Qy       561 LysGlyLysArgValLeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThr 580
Db      1870 AAAGGGAAGCGAGTTCTTTTCCTGACCAATGACTACTTCTTCACGGACATCAGCGACACC 1929

Qy       581 ProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsn 600
Db      1930 CCTTTCAGTTTGGGGGCGGTGCTGTCCCGGGGCCACGGAGAATACATCCTTCTGGGGAAC 1989

Qy       601 ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAsp 620
Db      1990 ACGTCTGTGGAAGAAGGCCTGCATGACTTGCTTCACCCAGACCTGGCCCTGGCCGGTGAC 2049

Qy       621 TrpIleTyrCysIleThrAspIleAspProAspHisArgLysLeuSerGlnLeuGluAla 640
Db      2050 TGGATCTACTGCATCACAGATATTGACCCAGACCACCGGAAGCTCAGCCAGCTAGAGGCC 2109

Qy       641 MetIleArgPheLeuThrArgLysAspProAspLeuGluCysAspGluGluLeuValArg 660
Db      2110 ATGATCCGCTTCCTCACCAGGAAGGACCCAGACCTGGAGTGTGACGAGGAGCTGGTCCGG 2169

Qy       661 GluValLeuPheAspAlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAla 680
Db      2170 GAGGTGCTGTTTGACGCGGTGGTGACAGCCCCCATGGAAGCCTACTGGACAGCGCTGGCC 2229

Qy       681 LeuAsnMetSerGluGluSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700
Db      2230 CTCAACATGTCCGAGGAGTCTGAACACGTGGTGGACATGGCCTTCCTGGGCACCCGGGCT 2289

Qy       701 GlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPheLeu 720
Db      2290 GGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGTCTCCGACAGGAAGTTCCTG 2349

Qy       721 ThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTrpTyrArgGln 740
Db      2350 ACACCTGAGGACGAGGCCAGCGTGTTCACCCTGGACCGCTTCCCGCTGTGGTACCGCCAG 2409

Qy       741 AlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGlu 760
Db      2410 GCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCTCCGCTGGGCAGAAGGACCAGAA 2469

Qy       761 SerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLys 780
Db      2470 AGTGCGGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGTGGCGGTGACCGTGGACAAG 2529

Qy       781 ArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLys 800
Db      2530 AGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAA 2589

Qy       801 PheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGlu 820
Db      2590 TTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCCGTACACACAGAGCTGCGAG 2649

Qy       821 AspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArg 840
Db      2650 GACAGTGATCTGGACTGCTTCGTCATCGACAACAACGGGTTCATTCTGATCTCCAAGAGG 2709

Qy       841 SerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeu 860
Db      2710 TCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGCTGTCCTGACCCAGCTGCTC 2769

Qy       861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
Db      2770 AGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCAGGCCATGTGCAAACCCTCG 2829

Qy       881 SerHisHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAla 900
Db      2830 AGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAATTTCTGCCTTCTTGACGGCG 2889

Qy       901 ThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySer 920
Db      2890 ACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGAGTGGAGTGTCTGGGGCTCC 2949

Qy       921 TrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLysLys 940
Db      2950 TGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCACTCCCACAAACACAAGAAG 3009

Qy       941 GlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAlaIle 960
Db      3010 CAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCAGCCGGCCATC 3069

Qy       961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGlnGln 980
Db      3070 CGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAAGGTATTTGTGGTGCAGCAG 3129

Qy       981 IleProAsnSerAsnLeuLeuLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
Db      3130 ATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCACCTGTGACTGCAGCATCTTC 3189

Qy      1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
Db      3190 CCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGCCTCTGTCAAATGTGACCGG 3249

Qy      1021 MetArgSerGlnLysLeuArgArgArgProAspSerCysHisAlaPheHisProGluVal 1040
Db      3250 ATGCGCTCCCAGAAGCTCCGCCGGCGACCAGACTCCTGCCACGCCTTCCATCCAGAGGTG 3309

Qy      1041 ArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGly 1060
Db      3310 CGGGTTGAGGCGGATCGAGGGTGGGCTGGATTTTCATCCCCAAACCCTCTGTGCCTGGGT 3369

Qy      1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
Db      3370 CTGTGCCCCTGCAGACAGGAGCATATAGGGATGCCAATGAACACACCTGTGCCTGTGCTT 3429

Qy      1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
Db      3430 CTCGGGGGAAACATTCGCGTTTATGCCCTG 3459
```

RESULT 3
AAA09254
ID AAA09254 standard; cDNA; 5073 BP.
XX
AC AAA09254;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human alpha-2-delta-D gene.
XX
KW alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   3. .3365
FT   /*tag= a
XX
PN WO200020450-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US023519.
XX
PR 07-OCT-1998; 98US-0103322P.
PR 30-OCT-1998; 98US-0106473P.
PR 29-DEC-1998; 98US-0114088P.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Johns MA, Moldover B, Offord JD;
XX
DR WPI; 2000-303744/26.

```
DR   P-PSDB; AAY92321.
XX
PT   New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT   proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT   anxiety, multiple sclerosis or cancer.
XX
PS   Claim 1; Page 64-66; 88pp; English.
XX
CC   The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC   The gene has been mapped to chromosome 12p13.1. This gene and the related
CC   alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC   from abnormal calcium flux by introducing expression vectors containing
CC   the respective gene into mammalian cells. The antisense genes are also
CC   useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC   is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC   Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
CC   related syndromes, migraine, ataxia, vestibular defects, chronic pain,
CC   sleep interference, anxiety, amyotropic lateral sclerosis (ALS), multiple
CC   sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
CC   syndromes, mood, depression or cancer
XX
SQ   Sequence 5073 BP; 1280 A; 1390 C; 1347 G; 1056 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0          Length:          5073
Score:                    5386.50    Matches:         1035
Percent Similarity:       97.47%     Conservative:    4
Best Local Similarity:    97.09%     Mismatches:      27
Query Match:              94.07%     Indels:          1
DB:                       3          Gaps:            0

US-09-833-222A-10 (1-1090) x AAA09254 (1-5073)

Qy          11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
               :::   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy          31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy          51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy          71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy          91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy         111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy         131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy         151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653

Qy         171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713

Qy         191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773

Qy         211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy         231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893

Qy         251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy         271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013

Qy         291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073

Qy         311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133

Qy         331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193

Qy         351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253

Qy         371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313

Qy         391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373

Qy         411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433

Qy         431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493

Qy         451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy         471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1554 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613

Qy         491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1614 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1673

Qy         511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1674 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1733

Qy         531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1734 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1793

Qy         551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1794 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 1853

Qy         571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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Db       1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913

Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610

Db       1914 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1973

Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630

Db       1974 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033

Qy        631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650

Db       2034 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2093

Qy        651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670

Db       2094 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2153

Qy        671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690

Db       2154 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2213

Qy        691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710

Db       2214 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2273

Qy        711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730

Db       2274 TCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACC 2333

Qy        731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750

Db       2334 CTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTC 2393

Qy        751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770

Db       2394 TTCAACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCA 2453

Qy        771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyVal 790

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Qy        791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810

Db       2514 CAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACT 2573

Qy        811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830

Db       2574 GTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGAC 2633

Qy        831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850

Db       2634 AACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 2693

Qy        851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870

Db       2694 GTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATG 2753

Qy        871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890

Db       2754 TATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTG 2813

Qy        891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910

Db       2814 GTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTG 2873

Qy        911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930

Db       2874 TTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGT 2933

Qy        931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950

Db       2934 GTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAG 2993

Qy        951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970

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Db       3054 CCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTG 3113

Qy        991 ThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010

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Qy       1011 LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgPro 1030

Db       3174 AAATATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACCA 3233

Qy       1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGly 1050

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Qy       1051 PheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070

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Qy       1071 MetProMetAsnThrPro 1076

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RESULT 4
ADE07110
ID ADE07110 standard; DNA; 4841 BP.
XX
AC ADE07110;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel coding sequence (useful for identifying genetic disorders) #176.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder; gene; ds.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
DR P-PSDB; ADE08021.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX

PS Claim 1; SEQ ID NO 176; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present DNA sequence represents a gene of the
CC invention.
XX
SQ Sequence 4841 BP; 1176 A; 1335 C; 1339 G; 991 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	4841
Score:	5385.50	Matches:	1034
Percent Similarity:	97.47%	Conservative:	5
Best Local Similarity:	97.00%	Mismatches:	27
Query Match:	94.05%	Indels:	1
DB:	10	Gaps:	0

US-09-833-222A-10 (1-1090) x ADE07110 (1-4841)

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Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 557

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 617

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 677

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 737

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
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Db        738 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 797

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 857

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 917

Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 977

Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 1037

Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
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Db       1098 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 1157

Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
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Db       1158 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 1217

Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||

Db       1218 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCATTAATATCATAGCGTACAATGAC 1277

Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1337

Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
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Db       1338 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1397

Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
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Qy        331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1458 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1517

Qy        351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1518 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1577

Qy        371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1637

Qy        391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1638 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1697

Qy        411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
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Qy        431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
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Db       1758 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1817

Qy        451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
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Db       1818 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1877

Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
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Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
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Db       1938 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1997

Qy        511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
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Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
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Db       2118 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 2177

Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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Db       2178 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 2237

Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
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Qy       631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
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Qy       811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db      2898 GTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGAC 2957

Qy       831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db      2958 AACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 3017

Qy       851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
Db      3018 GTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATG 3077

Qy       871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890
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Qy       891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910
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Qy       911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
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Qy       931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
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Qy       951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
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Qy       971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990
Db      3378 CCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTG 3437

Qy       991 ThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010
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Qy      1011 LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgPro 1030
Db      3498 AAATATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACCA 3557

Qy      1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGly 1050
Db      3558 GACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGCGGCGCCTCGGAC 3617

Qy      1051 PheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
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Qy      1071 MetProMetAsnThrPro 1076
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RESULT 5
AAS01433
ID AAS01433 standard; cDNA; 3339 BP.
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AC AAS01433;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #18 cDNA.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; ss.
XX
OS Homo sapiens.
XX
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FT   /note= "These two codons between them have an apparent 49
FT   nucleotide insertion which alters the reading frame"
XX
PN WO200119870-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP009137.
XX
PR 16-SEP-1999; 99US-00397550.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Brown JP, Bertelli F;
XX
DR WPI; 2001-235262/24.
DR P-PSDB; AAU01038.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays.
XX
PS Claim 39; Page 148-149; 160pp; English.
XX
CC The present sequence encodes for human secreted calcium channel
CC alpha2delta subunit #18 which is soluble and retains the functional

```
CC   characteristics of the full length or wild type alpha2delta subunit
CC   (AAU01025) from which it is derived. The invention relates to truncated
CC   alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC   which retain their affinity for radioactively labelled gabapentin. The
CC   alpha2delta subunit is 1 of the components of the heteromultimeric
CC   voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC   and non-neuronal tissues including heart and skeletal muscle. Numerous
CC   soluble forms of the human calcium channel alpha2delta subunits (AAU01014
CC   -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
CC   calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
CC   The secreted soluble alpha2delta subunit may be used in assays e.g.
CC   scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC   filter binding or wheat germ lectin flashplate assays to detect or
CC   measure the binding or interaction of a ligand (e.g. gabapentin, L-
CC   Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
CC   Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
CC   subunit
XX
SQ   Sequence 3339 BP; 780 A; 934 C; 960 G; 665 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0           Length:          3339
Score:                  5342.50     Matches:         1028
Percent Similarity:     97.54%      Conservative:    2
Best Local Similarity:  97.35%      Mismatches:      8
Query Match:            93.30%      Indels:          18
DB:                     4           Gaps:            2

US-09-833-222A-10 (1-1090) x AAS01433 (1-3339)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653

Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713

Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773

Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893

Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013

Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073

Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133

Qy        331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193

Qy        351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253

Qy        371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313

Qy        391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373

Qy        411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433

Qy        431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493

Qy        451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1554 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613

Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1614 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1673

Qy        511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1674 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1733

Qy        531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1734 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1793

Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1794 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 1853

Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913
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Qy       591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db      1914 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1973

Qy       611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db      1974 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033

Qy       631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db      2034 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2093

Qy       651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db      2094 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2153

Qy       671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db      2154 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2213

Qy       691 ValAspMetAlaPheLeuGlyThrArgAla---------------------------- 700
Db      2214 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2273

Qy       701 -------------------GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
Db      2274 TCCGAGAAGGTCTCCGAGTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGT 2333

Qy       714 lSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
Db      2334 CTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACCCTGGACCGCTT 2393

Qy       734 eProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
Db      2394 CCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCTCCG 2453

Qy       754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
Db      2454 CTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGT 2513

Qy       774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLe 794
Db      2514 GGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCT 2573

Qy       794 uGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814
Db      2574 GGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCC 2633

Qy       814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPh 834
Db      2634 GTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGACAACAACGGGTT 2693

Qy       834 eIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854
Db      2694 CATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGC 2753

Qy       854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
Db      2754 TGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCA 2813

Qy       874 nAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuValSerProIl 894
Db      2814 GGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAAT 2873

Qy       894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGl 914
Db      2874 TTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGA 2933

Qy       914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHi 934
Db      2934 GTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCA 2993

Qy       934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
```

```
Db      2994 CTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTT 3053

Qy       954 eValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLy 974
Db      3054 CGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAA 3113

Qy       974 sValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProTh 994
Db      3114 GGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCAC 3173

Qy       994 rCysAspCysSerIleProProValLeuGlnGluAlaThrGluValLysTyrAsnAl 1014
Db      3174 CTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGC 3233

Qy      1014 aSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgProAspSerCysHi 1034
Db      3234 CTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACCAGACTCCTGCCA 3293

Qy      1034 sAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
Db      3294 CGCCTTCCATCCAGAGGAGAATGCCCAG---GACTGCGGCGGCGCC 3336
```

RESULT 6
AAF57570
ID AAF57570 standard; DNA; 3339 BP.
XX
AC AAF57570;
XX
DT 11-JUN-2001 (first entry)
XX
DE Human calcium channel alpha2delta subunit encoding DNA.
XX
KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human; ds.
XX
OS Homo sapiens.
XX
PN WO200120336-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP009136.
XX
PR 16-SEP-1999; 99US-00397549.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
XX
DR WPI; 2001-257902/26.
XX
PT Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
PT the ligands identified are useful for treating disorders of the nervous
PT system, including pain.
XX
PS Disclosure; Page 146-147; 158pp; English.
XX
CC The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alpha2delta subunit encoding DNA
XX

SQ Sequence 3339 BP; 780 A; 934 C; 960 G; 665 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3339
Score:	5342.50	Matches:	1028
Percent Similarity:	97.54%	Conservative:	2
Best Local Similarity:	97.35%	Mismatches:	8
Query Match:	93.30%	Indels:	18
DB:	5	Gaps:	2

US-09-833-222A-10 (1-1090) x AAF57570 (1-3339)

```
Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653

Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713

Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773

Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893

Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013

Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073

Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133

Qy        331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193

Qy        351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253

Qy        371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313

Qy        391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
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Db       1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373

Qy        411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
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Db       1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433

Qy        431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
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Db       1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493

Qy        451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1554 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613

Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1614 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1673

Qy        511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1674 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1733

Qy        531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
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Db       1734 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1793

Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
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Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
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Db       1914 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1973

Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Db       1974 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033

Qy        631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
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Qy        671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
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Db       2154 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2213

Qy        691 ValAspMetAlaPheLeuGlyThrArgAla---------------------------- 700
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Db       2214 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2273

Qy        701 ------------------GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
                                 ||||||||||||||||||||||||||||||||||||||
Db       2274 TCCGAGAAGGTCTCCGAGTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGT 2333

Qy        714 lSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
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Qy        734 eProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
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Db       2394 CCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCTCCG 2453

Qy        754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
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Qy        774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLe 794
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Db       2514 GGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCT 2573

Qy        794 uGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814
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Db       2574 GGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCC 2633

Qy        814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPh 834
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Qy        834 eIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854
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Db       2694 CATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGC 2753

Qy        854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
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Db       2814 GGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAAT 2873

Qy        894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGl 914
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Db       2874 TTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGA 2933

Qy        914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHi 934
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Qy        934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
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Db       2994 CTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTT 3053

Qy        954 eValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLy 974
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Db       3054 CGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAA 3113

Qy        974 sValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProTh 994
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Db       3114 GGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCAC 3173

Qy        994 rCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyrAsnAl 1014
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Db       3174 CTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGC 3233

Qy       1014 aSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgProAspSerCysHi 1034
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Db       3234 CTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACCAGACTCCTGCCA 3293

Qy       1034 sAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
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Db       3294 CGCCTTCCATCCAGAGGAGAATGCCCAG---GACTGCGGCGGCGCC 3336
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RESULT 7
AAS01432
ID AAS01432 standard; cDNA; 3209 BP.
XX
AC AAS01432;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #17 cDNA.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   3. .3209
FT   /*tag= a
FT   /partial
FT   /product= "Alpha2delta calcium channel subunit #17"
FT   /note= "This sequence lacks a stop codon"
XX
PN WO200119870-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP009137.
XX
PR 16-SEP-1999; 99US-00397550.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Brown JP, Bertelli F;
XX
DR WPI; 2001-235262/24.
DR P-PSDB; AAU01037.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays.
XX
PS Claim 39; Page 147-148; 160pp; English.
XX
CC The present sequence encodes for human secreted calcium channel
CC alpha2delta subunit #17 which is soluble and retains the functional
CC characteristics of the full length or wild type alpha2delta subunit
CC (AAU01025) from which it is derived. The invention relates to truncated
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC which retain their affinity for radioactively labelled gabapentin. The
CC alpha2delta subunit is 1 of the components of the heteromultimeric
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits (AAU01014
CC -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
CC calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
CC The secreted soluble alpha2delta subunit may be used in assays e.g.
CC scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin, L-
CC Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
CC Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
CC subunit
XX
SQ Sequence 3209 BP; 757 A; 888 C; 920 G; 644 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3209
Score:	5276.00	Matches:	1008
Percent Similarity:	99.70%	Conservative:	1
Best Local Similarity:	99.60%	Mismatches:	3
Query Match:	92.14%	Indels:	0
DB:	4	Gaps:	0

US-09-833-222A-10 (1-1090) x AAS01432 (1-3209)

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Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
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Db        414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
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Db        474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
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Db        534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653

Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
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Db        654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713

Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773

Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
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Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
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Db        954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013

Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
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Db       1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073

Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
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Db       1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133

Qy        331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
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Db       1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193

Qy        351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
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Qy        371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
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Qy        391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
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Db       1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373

Qy        411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
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Db       1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433

Qy        431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493

Qy        451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
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Db       1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
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Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
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Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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Db       1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913

Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
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Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Qy        631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2034 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2093

Qy        651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
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Qy        671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
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Db       2154 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2213

Qy        691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
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Db       2214 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2273

Qy        711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730

Db       2274 TCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACC 2333

Qy        731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750

Db       2334 CTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTC 2393

Qy        751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770

Db       2394 TTCAACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCA 2453

Qy        771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyVal 790

Db       2454 AGCACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTC 2513

Qy        791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810

Db       2514 CAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACT 2573

Qy        811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830

Db       2574 GTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGAC 2633

Qy        831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850

Db       2634 AACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 2693

Qy        851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870

Db       2694 GTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATG 2753

Qy        871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890

Db       2754 TATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTG 2813

Qy        891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910

Db       2814 GTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTG 2873

Qy        911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930

Db       2874 TTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGT 2933

Qy        931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950

Db       2934 GTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAG 2993

Qy        951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970

Db       2994 TACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGG 3053

Qy        971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990

Db       3054 CCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTG 3113

Qy        991 ThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010

Db       3114 ACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGTC 3173

Qy       1011 LysTyrAsnAlaSerValLysCysAspArgMetArg 1022

Db       3174 AAATATAATGCCTCTGTCAAATGTGACCGGATGCGC 3209
```

```
RESULT 8
AAF57569
ID   AAF57569 standard; DNA; 3209 BP.
XX
AC   AAF57569;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Human calcium channel alpha2delta subunit encoding DNA.
XX
KW   Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW   nervous system disorder; pain; epilepsy; anxiety; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             3. .3209
FT                   /*tag=  a
XX
PN   WO200120336-A2.
XX
PD   22-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-EP009136.
XX
PR   16-SEP-1999;   99US-00397549.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bertelli F,  Brown JP,  Dissanayake V,  Suman-Chauhan N,  Gee NS;
XX
DR   WPI; 2001-257902/26.
DR   P-PSDB; AAB62261.
XX
PT   Competitive binding assay for screening ligands which bind a cerebral
PT   cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
PT   the ligands identified are useful for treating disorders of the nervous
PT   system, including pain.
XX
PS   Disclosure; Page 145-146; 158pp; English.
XX
CC   The invention relates to a new method for screening ligands which bind a
CC   cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC   preferably alpha2delta-1 subunit. The method comprises contacting a
CC   secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC   interest and a labelled compound which binds the subunit, followed by
CC   measuring the level of binding of the labelled compound to alpha2delta-1
CC   subunit. The method is useful for screening ligands, preferably
CC   biologically active products that modulate a nervous system function,
CC   which bind a cerebral cortical voltage-dependent calcium channel
CC   alpha2delta-1 subunit. The ligands identified by the method are useful
CC   for treating disorders of the nervous system, including pain, epilepsy
CC   and anxiety. The present sequence represents a human calcium channel
CC   alpha2delta subunit encoding DNA
XX
SQ   Sequence 3209 BP; 757 A; 888 C; 920 G; 644 T; 0 U; 0 Other;
```

Alignment Scores:			
Pred. No.:	0	Length:	3209
Score:	5276.00	Matches:	1008
Percent Similarity:	99.70%	Conservative:	1
Best Local Similarity:	99.60%	Mismatches:	3
Query Match:	92.14%	Indels:	0
DB:	5	Gaps:	0

US-09-833-222A-10 (1-1090) x AAF57569 (1-3209)

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Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30

Db        174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50

Db        234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70

Db        294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353
```

```
Qy        71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
Db       354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy        91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
Db       414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy       111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
Db       474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy       131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
Db       534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy       151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db       594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653

Qy       171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
Db       654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713

Qy       191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
Db       714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773

Qy       211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
Db       774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy       231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db       834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893

Qy       251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db       894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy       271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
Db       954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013

Qy       291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
Db      1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073

Qy       311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db      1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133

Qy       331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db      1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193

Qy       351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db      1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTCACTTACCTCATTGGGAGA 1253

Qy       371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db      1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313

Qy       391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
Db      1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373

Qy       411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
Db      1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433

Qy       431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450

Db      1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493

Qy       451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db      1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy       471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Db      1554 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613

Qy       491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
Db      1614 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1673

Qy       511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
Db      1674 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1733

Qy       531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db      1734 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1793

Qy       551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db      1794 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 1853

Qy       571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db      1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913

Qy       591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db      1914 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1973

Qy       611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db      1974 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033

Qy       631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db      2034 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2093

Qy       651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db      2094 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2153

Qy       671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db      2154 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2213

Qy       691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
Db      2214 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2273

Qy       711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
Db      2274 TCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACC 2333

Qy       731 LeuAspArgProProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750
Db      2334 CTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTC 2393

Qy       751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
Db      2394 TTCAACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCA 2453

Qy       771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyVal 790
Db      2454 AGCACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTC 2513

Qy       791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
```

```
Db       2514 CAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACT 2573

Qy        811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db       2574 GTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGAC 2633

Qy        831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2634 AACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 2693

Qy        851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2694 GTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATG 2753

Qy        871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2754 TATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTG 2813

Qy        891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2814 GTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTG 2873

Qy        911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2874 TTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGT 2933

Qy        931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2934 GTCTTCCATCACTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAG 2993

Qy        951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2994 TACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGG 3053

Qy        971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3054 CCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTG 3113

Qy        991 ThrAspProThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3114 ACAGACCCCACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGTC 3173

Qy       1011 LysTyrAsnAlaSerValLysCysAspArgMetArg 1022
              |||||||||||||||||||||||||||||||||||
Db       3174 AAATATAATGCCTCTGTCAAATGTGACCGGATGCGC 3209
```

```
RESULT 9
AAS17581
ID   AAS17581 standard; cDNA; 3228 BP.
XX
AC   AAS17581;
XX
DT   26-FEB-2002  (first entry)
XX
DE   DNA encoding novel secreted protein #10.
XX
KW   Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine;
KW   antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human;
KW   cancer; autoimmune disease; wound healing disorder; infection;
KW   haematopoietic disorder; inflammatory disorder; infertility;
KW   neurological disease; psychiatric disease; cardiovascular disease;
KW   respiratory disease; renal; gastrointestinal; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3228
FT                   /*tag=  a
FT                   /product= "Human secreted protein"
XX
PN   WO200179454-A1.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US011797.
XX
PR   13-APR-2000; 2000US-0196603P.
PR   24-APR-2000; 2000US-0199417P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Agarwal P,  Murdoch PR,  Rizvi SK,  Smith RF,  Xiang Z;
XX
DR   WPI; 2002-061975/08.
DR   P-PSDB; AAU09869.
XX
PT   New secreted proteins or polypeptides, useful for treating e.g. cancer,
PT   autoimmune diseases, wound healing disorder, infections, hematopoietic
PT   disorders, inflammatory disorders, infertility, cancer.
XX
PS   Claim 2; Page 41-42; 92pp; English.
XX
CC   The invention relates to an isolated novel secreted polypeptide (I) and
CC   polynucleotide (II). (I) and (II) are useful for treating cancer,
CC   autoimmune diseases, wound healing disorder, infections, haematopoietic
CC   disorders, inflammatory disorders, infertility, neurological and
CC   psychiatric diseases, cardiovascular diseases, respiratory diseases,
CC   renal diseases, or gastrointestinal diseases. These may also be used to
CC   treat diseases, abnormalities and disorders caused by abnormal
CC   expression, production, function and/or metabolism of the genes, as
CC   vaccines for inducing immunological response in a mammal, and in
CC   screening methods for detecting the effect of added compounds on the
CC   production of mRNA and polypeptide in cells. The polypeptides can be used
CC   as immunogens to produce antibodies immunospecific for the polypeptides,
CC   and to identify membrane-bound or soluble receptors. The polynucleotides
CC   may be used as diagnostic reagents, in chromosome localisation studies,
CC   and in tissue expression studies. The present sequence represents the
CC   coding sequence of novel human secreted protein #10
XX
SQ   Sequence 3228 BP; 749 A; 897 C; 932 G; 650 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.:              0               Length:         3228
Score:                  5234.50         Matches:        1013
Percent Similarity:     95.68%          Conservative:   7
Best Local Similarity:  95.03%          Mismatches:     34
Query Match:            91.42%          Indels:         13
DB:                     6               Gaps:           3

US-09-833-222A-10 (1-1090) x AAS17581 (1-3228)

Qy         12 ArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyr 31
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 AGAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAATAC 117

Qy         32 SerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGlu 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATCGAG 177

Qy         52 GluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTGCGG 237

Qy         72 ArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHis 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAACCAC 297

Qy         92 GluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAsp 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGGGAC 357

Qy        112 GluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPhe 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 GAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCACTTC 417
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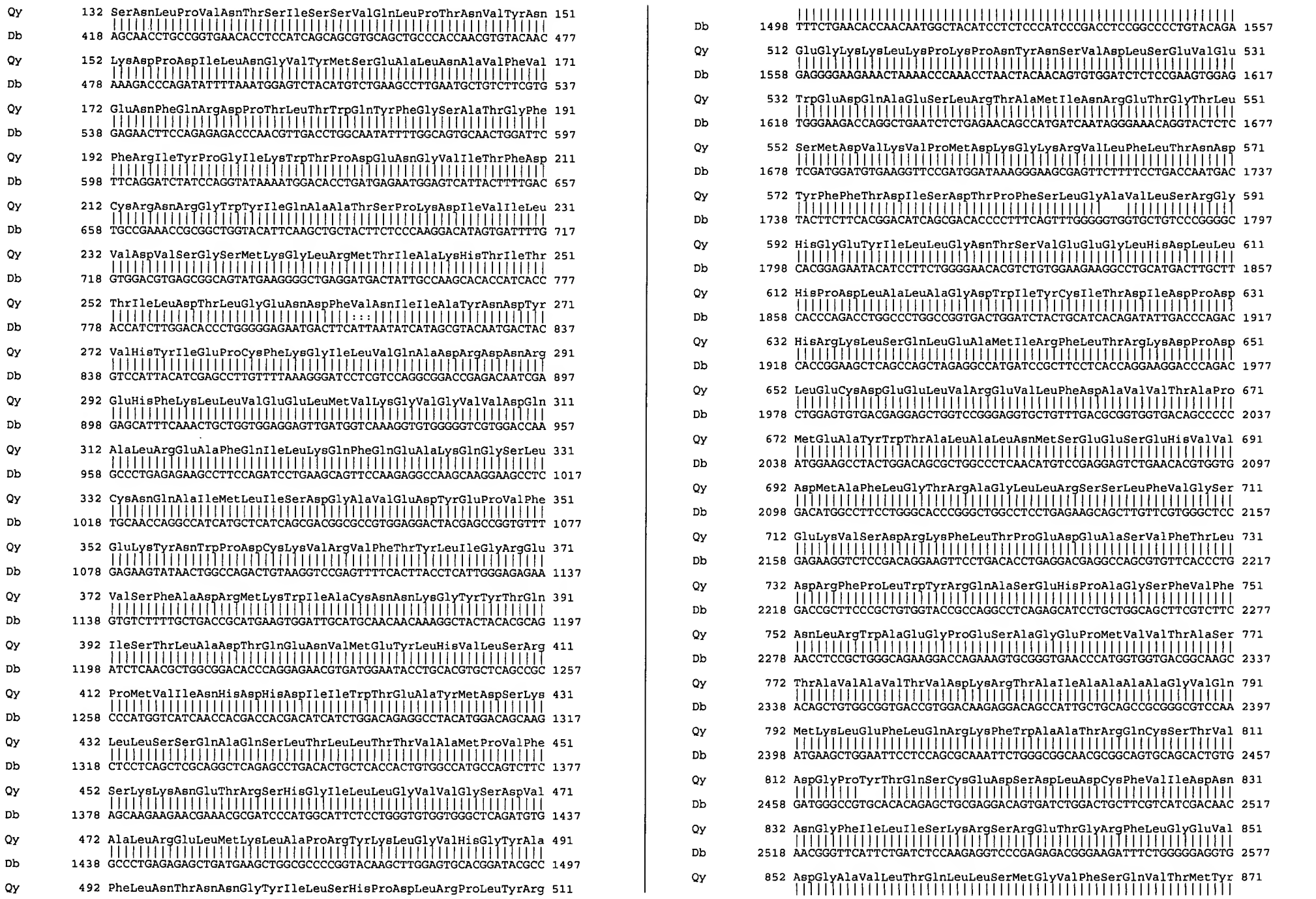
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Db 418 AGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTACAAC 477
Qy 152 LysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheVal 171
Db 478 AAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTCGTG 537
Qy 172 GluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhe 191
Db 538 GAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGATTC 597
Qy 192 PheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAsp 211
Db 598 TTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTTGAC 657
Qy 212 CysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeu 231
Db 658 TGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATTTTG 717
Qy 232 ValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251
Db 718 GTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATCACC 777
Qy 252 ThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyr 271
Db 778 ACCATCTTGGACACCCTGGGGGAGAATGACTTCATTAATATCATAGCGTACAATGACTAC 837
Qy 272 ValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArg 291
Db 838 GTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAATCGA 897
Qy 292 GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGln 311
Db 898 GAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGACCAA 957
Qy 312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeu 331
Db 958 GCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGCCTC 1017
Qy 332 CysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPhe 351
Db 1018 TGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTGTTT 1077
Qy 352 GluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGlu 371
Db 1078 GAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGAGAA 1137
Qy 372 ValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGln 391
Db 1138 GTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACGCAG 1197
Qy 392 IleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArg 411
Db 1198 ATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGCCGC 1257
Qy 412 ProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLys 431
Db 1258 CCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGCAAG 1317
Qy 432 LeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPhe 451
Db 1318 CTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTCTTC 1377
Qy 452 SerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspVal 471
Db 1378 AGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGATGTG 1437
Qy 472 AlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAla 491
Db 1438 GCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATACGCC 1497
Qy 492 PheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArg 511
Db 1498 TTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTACAGA 1557
Qy 512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
Db 1558 GAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTGGAG 1617
Qy 532 TrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeu 551
Db 1618 TGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACTCTC 1677
Qy 552 SerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAsp 571
Db 1678 TCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAATGAC 1737
Qy 572 TyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGly 591
Db 1738 TACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGGGGC 1797
Qy 592 HisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeu 611
Db 1798 CACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTGCTT 1857
Qy 612 HisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAsp 631
Db 1858 CACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCAGAC 1917
Qy 632 HisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp 651
Db 1918 CACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCAGAC 1977
Qy 652 LeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaPro 671
Db 1978 CTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCCCCC 2037
Qy 672 MetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValVal 691
Db 2038 ATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTGGTG 2097
Qy 692 AspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySer 711
Db 2098 GACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCC 2157
Qy 712 GluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeu 731
Db 2158 GAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACCCTG 2217
Qy 732 AspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPhe 751
Db 2218 GACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTC 2277
Qy 752 AsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSer 771
Db 2278 AACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCAAGC 2337
Qy 772 ThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGln 791
Db 2338 ACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAA 2397
Qy 792 MetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrVal 811
Db 2398 ATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACTGTG 2457
Qy 812 AspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsn 831
Db 2458 GATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGACAAC 2517
Qy 832 AsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluVal 851
Db 2518 AACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTG 2577
Qy 852 AspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyr 871

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Db       2578 GATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTAT 2637

Qy        872 AspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuVal 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2638 GACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTC 2697

Qy        892 SerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPhe 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2698 AGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTC 2757

Qy        912 LeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerVal 931
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2758 CTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCC--------- 2808

Qy        932 PheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyr 951
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2809 ------------CACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTAC 2856

Qy        952 ProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyPro 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2857 CCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCC 2916

Qy        972 CysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThr 991
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2917 TGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACA 2976

Qy        992 AspProThr---CysAspCysSerIleProProValLeuGlnGluAlaThrGluVal 1010
              |||||||||   |||                 |||   :::|||
Db       2977 GACCCCACCTTCTGCAGAATGGGCTCCGGTCCTGAGATATTGACCTTAACAGTGGCTTCT 3036

Qy       1011 LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgPro 1030
                :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3037 GCACATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACCA 3096

Qy       1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGly 1050
              ||||||||||||||||||||||||||         :::         |||   :::
Db       3097 GACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGCGGCGCCTCGGAC 3156

Qy       1051 PheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
                |||:::      ||||||   |||      |||   |||             :::|||
Db       3157 ACCTCAGCCTCGCCGCCCCTACTCCTGCT-GCCTGTGTGTGC-----------CTGGGG 3203

Qy       1071 MetProMetAsnThrPro 1076
                     ||||||
Db       3204 GCTACTGCCCCAACTCCT 3221
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```
RESULT 10
AAS17582
ID   AAS17582 standard; cDNA; 3345 BP.
XX
AC   AAS17582;
XX
DT   26-FEB-2002  (first entry)
XX
DE   DNA encoding novel secreted protein #11.
XX
KW   Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine;
KW   antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human;
KW   cancer; autoimmune disease; wound healing disorder; infection;
KW   haematopoietic disorder; inflammatory disorder; infertility;
KW   neurological disease; psychiatric disease; cardiovascular disease;
KW   respiratory disease; renal; gastrointestinal; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3345
FT                   /*tag= a
FT                   /product= "Human secreted protein"
XX
PN   WO200179454-A1.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US011797.
XX
PR   13-APR-2000; 2000US-0196603P.
PR   24-APR-2000; 2000US-0199417P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Agarwal P,  Murdoch PR,  Rizvi SK,  Smith RF,  Xiang Z;
XX
DR   WPI; 2002-061975/08.
DR   P-PSDB; AAU09870.
XX
PT   New secreted proteins or polypeptides, useful for treating e.g. cancer,
PT   autoimmune diseases, wound healing disorder, infections, hematopoietic
PT   disorders, inflammatory disorders, infertility, cancer.
XX
PS   Claim 2; Page 42-44; 92pp; English.
XX
CC   The invention relates to an isolated novel secreted polypeptide (I) and
CC   polynucleotide (II). (I) and (II) are useful for treating cancer,
CC   autoimmune diseases, wound healing disorder, infections, haematopoietic
CC   disorders, inflammatory disorders, infertility, neurological and
CC   psychiatric diseases, cardiovascular diseases, respiratory diseases,
CC   renal diseases, or gastrointestinal diseases. These may also be used to
CC   treat diseases, abnormalities and disorders caused by abnormal
CC   expression, production, function and/or metabolism of the genes, as
CC   vaccines for inducing immunological response in a mammal, and in
CC   screening methods for detecting the effect of added compounds on the
CC   production of mRNA and polypeptide in cells. The polypeptides can be used
CC   as immunogens to produce antibodies immunospecific for the polypeptides,
CC   and to identify membrane-bound or soluble receptors. The polynucleotides
CC   may be used as diagnostic reagents, in chromosome localisation studies,
CC   and in tissue expression studies. The present sequence represents the
CC   coding sequence of novel human secreted protein #11
XX
SQ   Sequence 3345 BP; 772 A; 943 C; 960 G; 670 T; 0 U; 0 Other;
```

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Alignment Scores:
Pred. No.:                0                 Length:          3345
Score:                    5230.50           Matches:         1012
Percent Similarity:       95.60%            Conservative:    8
Best Local Similarity:    94.85%            Mismatches:      35
Query Match:              91.35%            Indels:          13
DB:                       6                 Gaps:            3

US-09-833-222A-10 (1-1090) x AAS17582 (1-3345)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
                :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 231

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 291

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 351

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 411

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 471

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 531
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Qy       131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
Db       532 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 591

Qy       151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db       592 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 651

Qy       171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
Db       652 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 711

Qy       191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
Db       712 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 771

Qy       211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
Db       772 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 831

Qy       231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db       832 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 891

Qy       251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db       892 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCATTAATATCATAGCGTACAATGAC 951

Qy       271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
Db       952 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1011

Qy       291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
Db      1012 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1071

Qy       311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db      1072 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1131

Qy       331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db      1132 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1191

Qy       351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db      1192 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1251

Qy       371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db      1252 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1311

Qy       391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
Db      1312 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1371

Qy       411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
Db      1372 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1431

Qy       431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
Db      1432 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1491

Qy       451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db      1492 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1551

Qy       471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Db      1552 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1611

Qy       491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
Db      1612 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1671

Qy       511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
Db      1672 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1731

Qy       531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db      1732 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1791

Qy       551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db      1792 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 1851

Qy       571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db      1852 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1911

Qy       591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db      1912 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1971

Qy       611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db      1972 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2031

Qy       631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db      2032 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2091

Qy       651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db      2092 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2151

Qy       671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db      2152 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2211

Qy       691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
Db      2212 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2271

Qy       711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
Db      2272 TCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACC 2331

Qy       731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750
Db      2332 CTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTC 2391

Qy       751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
Db      2392 TTCAACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCA 2451

Qy       771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyVal 790
Db      2452 AGCACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTC 2511

Qy       791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
Db      2512 CAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACT 2571

Qy       811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db      2572 GTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGAC 2631

Qy       831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db      2632 AACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 2691

Qy       851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
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Db       2692 GTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATG 2751

Qy        871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2752 TATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTG 2811

Qy        891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2812 GTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTG 2871

Qy        911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2872 TTCCTGCTGGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCC------ 2925

Qy        931 ValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGlu 950
                          ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2926 --------------CACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAG 2970

Qy        951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2971 TACCCCGTGTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGG 3030

Qy        971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuVal 990
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3031 CCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTG 3090

Qy        991 ThrAspProThr---CysAspCysSerIleProProValLeuGlnGluAlaThrGlu 1009
              ||||||||||||   |||                |||   :::|||
Db       3091 ACAGACCCCACCTTCTGCAGAATGGGCTCCGGTCCTGAGATATTGACCTTAACAGTGGCT 3150

Qy       1010 ValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArg 1029
                 :::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3151 TCTGCACATAATGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGA 3210

Qy       1030 ProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
              ||||||||||||||||||||||||||||||        :::          |||   :::
Db       3211 CCAGACTCCTGCCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGCGGCGCCTCG 3270

Qy       1050 GlyPheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIle 1069
                 |||:::      ||||||  |||      |||   |||                :::
Db       3271 GACACCTCAGCCTCGCCGCCCCTACTCCTGCT-GCCTGTGTGTGC-----------CTG 3317

Qy       1070 GlyMetProMetAsnThrPro 1076
              |||          ||||||
Db       3318 GGGGCTACTGCCCCAACTCCT 3338

RESULT 11
AAA09278
ID   AAA09278 standard; cDNA; 5713 BP.
XX
AC   AAA09278;
XX
DT   10-AUG-2000  (first entry)
XX
DE   Human alpha-2-delta-D gene splice variant 2.
XX
KW   alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
KW   anticonvulsant; antimigrane; antiparkinsonian; antidepressant;
KW   splice variant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             3. .3293
FT                   /*tag= a
FT                   /transl_except= (pos:930. .932, aa:Xaa)
FT                   /note= "Xaa not defined"
XX
PN   WO200020450-A2.
XX
PD   13-APR-2000.
XX
PF   07-OCT-1999;   99WO-US023519.
XX
PR   07-OCT-1998;   98US-0103322P.
PR   30-OCT-1998;   98US-0106473P.
PR   29-DEC-1998;   98US-0114088P.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Johns MA,  Moldover B,  Offord JD;
XX
DR   WPI; 2000-303744/26.
DR   P-PSDB; AAY92323.
XX
PT   New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT   proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT   anxiety, multiple sclerosis or cancer.
XX
PS   Claim 22; Page 71-72; 88pp; English.
XX
CC   The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC   The gene has been mapped to chromosome 12p13.1. This gene and the related
CC   alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC   from abnormal calcium flux by introducing expression vectors containing
CC   the respective gene into mammalian cells. The antisense genes are also
CC   useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC   is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC   Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
CC   related syndromes, migraine, ataxia, vestibular defects, chronic pain,
CC   sleep interference, anxiety, amyotropic lateral sclerosis (ALS), multiple
CC   sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
CC   syndromes, mood, depression or cancer
XX
SQ   Sequence 5713 BP; 1397 A; 1570 C; 1548 G; 1195 T; 0 U; 3 Other;

Alignment Scores:
Pred. No.:                0                 Length:          5713
Score:                    5197.50           Matches:         1032
Percent Similarity:       80.87%            Conservative:    4
Best Local Similarity:    80.56%            Mismatches:      30
Query Match:              90.77%            Indels:          217
DB:                       3                 Gaps:            2

US-09-833-222A-10 (1-1090) x AAA09278 (1-5713)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
                 :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy         91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy        111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy        131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy        151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653
Qy        171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
Db        654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713
Qy        191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
Db        714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773
Qy        211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
Db        774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833
Qy        231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db        834 TTGGTGGACGTGAGCGGCAGTATGAAGGGCTGAGGATGACTATTGCCAAGCACACCATC 893
Qy        251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db        894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCRTTAATATCATAGCGTACAATGAC 953
Qy        271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
Db        954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013
Qy        291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
Db       1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073
Qy        311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db       1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133
Qy        331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db       1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193
Qy        351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db       1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253
Qy        371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db       1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313
Qy        391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
Db       1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373
Qy        411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
Db       1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433
Qy        431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
Db       1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493
Qy        451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db       1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553
Qy        471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Db       1554 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613
Qy        491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
Db       1614 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1673
Qy        511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
Db       1674 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1733

Qy        531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db       1734 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1793
Qy        551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db       1794 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 1853
Qy        571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db       1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913
Qy        591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db       1914 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1973
Qy        611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db       1974 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033
Qy        631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db       2034 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2093
Qy        651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db       2094 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2153
Qy        671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db       2154 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2213
Qy        691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
Db       2214 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2273
Qy        711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
Db       2274 TCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACC 2333
Qy        731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750
Db       2334 CTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTC 2393
Qy        751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
Db       2394 TTCAACCTCCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCA 2453
Qy        771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyVal 790
Db       2454 AGCACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTC 2513
Qy        791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
Db       2514 CAAATGAAGCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACT 2573
Qy        811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db       2574 GTGGATGGGCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGAC 2633
Qy        831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db       2634 AACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 2693
Qy        851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
Db       2694 GTGGATGGTGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATG 2753
Qy        871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890
Db       2754 TATGACTATCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTG 2813
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Qy       891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910
Db      2814 GTCAGCCCAATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCT- 2872

Qy       910 ------------------------------------------------------------ 910

Db      2873 TGTGAGTGGGGGTAGACACGGGGCTGGTGGAGGCTGCATGCGAGGGTGGCTTAGGAGGGT 2932

Qy       910 ------------------------------------------------------------ 910

Db      2933 GTCCTTGATCAGGAGGCTGCAAGGTCTCCAGGACAACCCACTTGCTACCAAGACCCCGGG 2992

Qy       910 ------------------------------------------------------------ 910

Db      2993 GAAGGAGGGCACAATCCCTGGGCATGGACGCCACCTCTTCCCTGCATGCTTGCCCCTGGG 3052

Qy       910 ------------------------------------------------------------ 910

Db      3053 AGGGACCTCATTGCTCAACCAGAGCCCTCAAGCAGGGAAGAGGGTGTCCTGGAGGAGAGG 3112

Qy       910 ------------------------------------------------------------ 910

Db      3113 GGATGGGCCGGGGGCTGTCAGGGATACTCCAGCTCCTTGGGAACCCAAGTCGGGAGGGCT 3172

Qy       911 -----------------------------------PheLeuLeuGluTrpSerValTrp 918
                                                 ||||||||||||||||||||||||
Db      3173 CAGAGGTCTCCGAGATTCAGTCCTGTGTCTGACAGGTTCCTGCTGGAGTGGAGTGTCTGG 3232

Qy       919 GlySerTrpTyrAspArgGlyAlaGlu--------------------------------- 927
             |||||||||||||||||||||||||
Db      3233 GGCTCCTGGTACGACAGAGGGGCCGAGGGTGAGTGCACGGAGCTGCAGGGCCATGTGCTG 3292

Qy       927 ------------------------------------------------------------ 927

Db      3293 AAGAGCAGTGGCATTTTGGTCCACTAACGTGAGACCATTCCCTGTGGGGTGGGTGACAGT 3352

Qy       927 ------------------------------------------------------------ 927

Db      3353 GGGGATAGGTGACCCTGAAGCATCGTTGTTCACATCTCACCCTGCGTGGCCTTCTCTCAT 3412

Qy       927 ------------------------------------------------------------ 927

Db      3413 CACATCCCTCACTCCTGGCTCTGTGTGTGACATCATCTTGGGACACCGCCACTCCATGTG 3472

Qy       927 ------------------------------------------------------------ 927

Db      3473 CCATCATCACCACCCCATGACATCCTGCCCTCATGTGCCACCATGTTTTCCTGTGCCGTG 3532

Qy       928 ------------------------------AlaLysSerValPheHisHisSerHisLy 937
                                           ||||||||||||||||||||||||||||||
Db      3533 TCCACCCTGTGCTGGGCTTATGTTCCGGCCAGCCAAAAGTGTCTTCCATCACTCCCACAA 3592

Qy       937 sHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGl 957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3593 ACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTTCGTGTACCA 3652

Qy       957 nPro-AlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheV 977
             ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3653 GCCGGNCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAAGGTATTTG 3712

Qy       977 alValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProThrCysAspC 997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3713 TGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCACCTGTGACT 3772

Qy       997 ysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValL 1017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3773 GCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAATGCCTCTGTCA 3832

Qy      1017 ysCysAspArgMetArgSerGlnLysLeuArgArgArgProAspSerCysHisAlaPheH 1037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3833 AATGTGACCGGATGCGCTCCCAGAAGCTCCGCCGGCGACCAGACTCCTGCCACGCCTTCC 3892

Qy      1037 isProGluValArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProL 1057
             ||||||||        :::         |||   :::      |||:::      ||||
Db      3893 ATCCAGAGGAGAATGCCCAGGACTGCGGYGGCGCCTCGGACACCTCAGCCTCGCCGCCCC 3952

Qy      1057 euCysLeuGlyLeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrPro 1076
             ||   |||      |||   |||                 |||      ||||||
Db      3953 TACTCCTGCT-GCCTGTGTGTGCCTGGGGGCTACTGCCCCAACTCCTGCGGTGACACCA 4010
```

RESULT 12
AAS01431
ID AAS01431 standard; cDNA; 3201 BP.
XX
AC AAS01431;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #16 cDNA.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   3. .3201
FT   /*tag= a
FT   /partial
FT   /product= "Alpha2delta calcium channel subunit #16"
FT   /note= "This sequence lacks a stop codon"
FT   /transl_except= (pos:2286. .2340,aa:Ser-Asp)
FT   /note= "These two codons between them have an apparent 49
FT   nucleotide insertion which alters the reading frame"
XX
PN WO200119870-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP009137.
XX
PR 16-SEP-1999; 99US-00397550.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Brown JP, Bertelli F;
XX
DR WPI; 2001-235262/24.
DR P-PSDB; AAU01036.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays.
XX
PS Claim 39; Page 146-147; 160pp; English.
XX
CC The present sequence encodes for human secreted calcium channel
CC alpha2delta subunit #16 which is soluble and retains the functional
CC characteristics of the full length or wild type alpha2delta subunit
CC (AAU01025) from which it is derived. The invention relates to truncated
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC which retain their affinity for radioactively labelled gabapentin. The
CC alpha2delta subunit is 1 of the components of the heteromultimeric
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits (AAU01014
CC -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
CC calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
CC The secreted soluble alpha2delta subunit may be used in assays e.g.
CC scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin, L-
CC Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
CC Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta

```
CC   subunit
XX
SQ   Sequence 3201 BP; 748 A; 888 C; 921 G; 644 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0              Length:          3201
Score:                    5148.00        Matches:         989
Percent Similarity:       98.02%         Conservative:    1
Best Local Similarity:    97.92%         Mismatches:      3
Query Match:              89.91%         Indels:          17
DB:                       4              Gaps:            1

US-09-833-222A-10 (1-1090) x AAS01431 (1-3201)

Qy          11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
               :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy          31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy          51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353

Qy          71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413

Qy          91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473

Qy         111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533

Qy         131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593

Qy         151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653

Qy         171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713

Qy         191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773

Qy         211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833

Qy         231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893

Qy         251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953

Qy         271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         954 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 1013

Qy         291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1014 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1073

Qy         311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133

Qy         331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1134 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1193

Qy         351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253

Qy         371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313

Qy         391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373

Qy         411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
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Db        1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433

Qy         431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493

Qy         451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553

Qy         471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1614 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1673

Qy         511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
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Db        1674 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1733

Qy         531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1734 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1793

Qy         551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1794 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 1853

Qy         571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
               ||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db        1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913

Qy         591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1914 GGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTG 1973

Qy         611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Db        1974 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033

Qy         631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2034 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2093

Qy         651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2094 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2153
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Qy        671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
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Db       2154 CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2213

Qy        691 ValAspMetAlaPheLeuGlyThrArgAla---------------------------- 700
              ||||||||||||||||||||||||||||
Db       2214 GTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGC 2273

Qy        701 ------------------GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
                                 ||||||||||||||||||||||||||||||||||||||||
Db       2274 TCCGAGAAGGTCTCCGAGTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGT 2333

Qy        714 iSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
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Qy        734 eProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
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Db       2394 CCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCTCCG 2453

Qy        754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
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Db       2454 CTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGT 2513

Qy        774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLe 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2514 GGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCT 2573

Qy        794 uGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2574 GGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCC 2633

Qy        814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPh 834
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2634 GTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGACAACAACGGGTT 2693

Qy        834 eIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854
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Db       2694 CATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGC 2753

Qy        854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2754 TGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCA 2813

Qy        874 nAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuValSerProIl 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2814 GGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAAT 2873

Qy        894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGl 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2874 TTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGA 2933

Qy        914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHi 934
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2934 GTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCA 2993

Qy        934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2994 CTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTT 3053

Qy        954 eValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLy 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3054 CGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAA 3113

Qy        974 sValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProTh 994
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3114 GGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCAC 3173

Qy        994 rCysAspCysSerIleProProVal 1003
              |||||||||||||||||||||||||
Db       3174 CTGTGACTGCAGCATCTTCCCACCAGTG 3201
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RESULT 13

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AAF57568
ID   AAF57568 standard; DNA; 3201 BP.
XX
AC   AAF57568;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Human calcium channel alpha2delta subunit encoding DNA.
XX
KW   Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW   nervous system disorder; pain; epilepsy; anxiety; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO200120336-A2.
XX
PD   22-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-EP009136.
XX
PR   16-SEP-1999;   99US-00397549.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bertelli F,  Brown JP,  Dissanayake V,  Suman-Chauhan N,  Gee NS;
XX
DR   WPI; 2001-257902/26.
XX
PT   Competitive binding assay for screening ligands which bind a cerebral
PT   cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
PT   the ligands identified are useful for treating disorders of the nervous
PT   system, including pain.
XX
PS   Disclosure; Page 144-145; 158pp; English.
XX
CC   The invention relates to a new method for screening ligands which bind a
CC   cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC   preferably alpha2delta-1 subunit. The method comprises contacting a
CC   secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC   interest and a labelled compound which binds the subunit, followed by
CC   measuring the level of binding of the labelled compound to alpha2delta-1
CC   subunit. The method is useful for screening ligands, preferably
CC   biologically active products that modulate a nervous system function,
CC   which bind a cerebral cortical voltage-dependent calcium channel
CC   alpha2delta-1 subunit. The ligands identified by the method are useful
CC   for treating disorders of the nervous system, including pain, epilepsy
CC   and anxiety. The present sequence represents a human calcium channel
CC   alpha2delta subunit encoding DNA
XX
SQ   Sequence 3201 BP; 748 A; 888 C; 921 G; 644 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:	0	Length:	3201
Score:	5148.00	Matches:	989
Percent Similarity:	98.02%	Conservative:	1
Best Local Similarity:	97.92%	Mismatches:	3
Query Match:	89.91%	Indels:	17
DB:	5	Gaps:	1

US-09-833-222A-10 (1-1090) x AAF57568 (1-3201)

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Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 293

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 353
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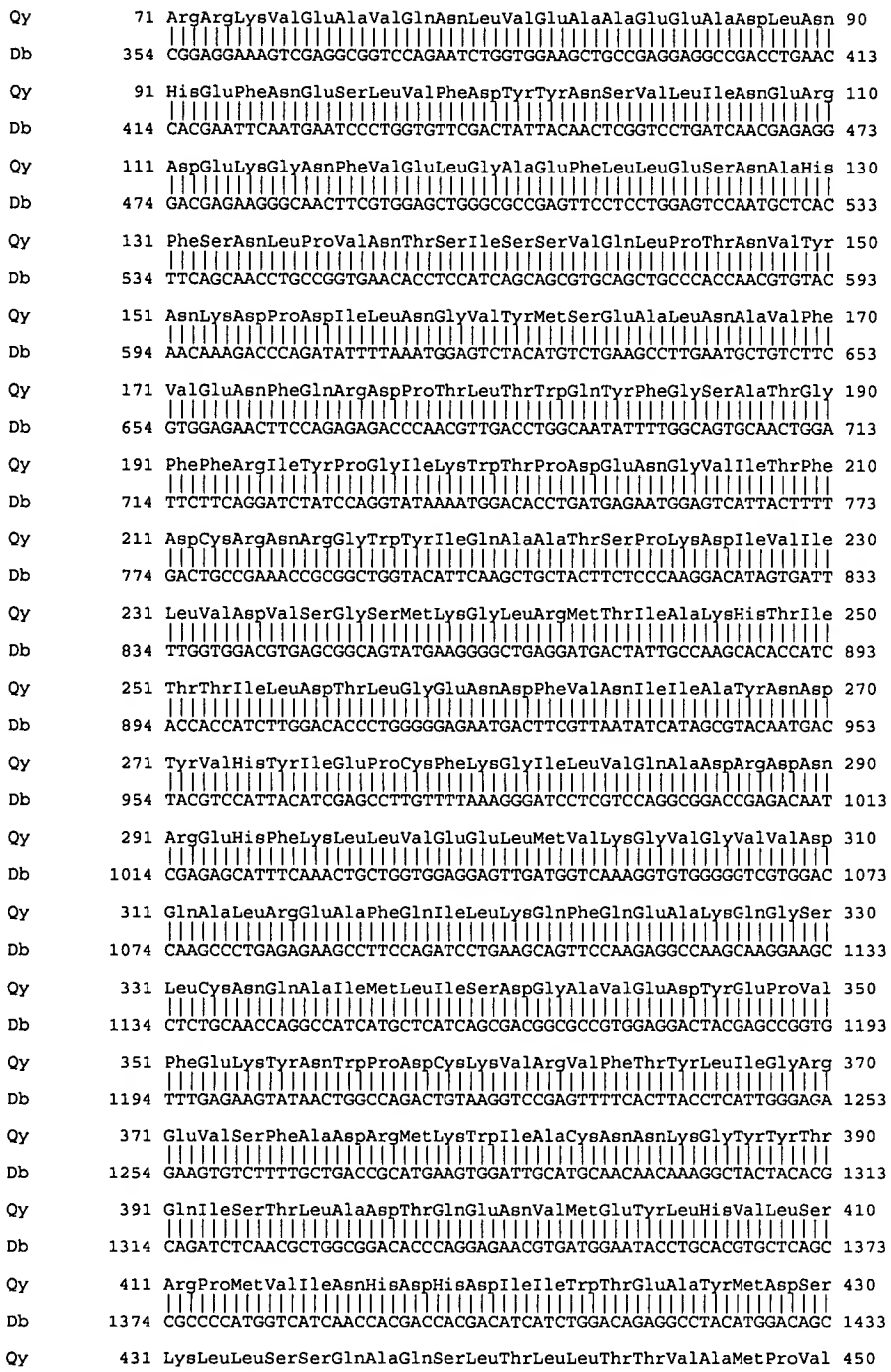
Qy 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
Db 354 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 413
Qy 91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
Db 414 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 473
Qy 111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
Db 474 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 533
Qy 131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
Db 534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 593
Qy 151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db 594 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653
Qy 171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
Db 654 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 713
Qy 191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
Db 714 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 773
Qy 211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
Db 774 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833
Qy 231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db 834 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 893
Qy 251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db 894 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 953
Qy 271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
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Qy 311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db 1074 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1133
Qy 331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
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Qy 351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db 1194 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1253
Qy 371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db 1254 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1313
Qy 391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
Db 1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373
Qy 411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
Db 1374 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1433
Qy 431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
Db 1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCAGTC 1493
Qy 451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db 1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1553
Qy 471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Db 1554 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613
Qy 491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
Db 1614 GCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTAC 1673
Qy 511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
Db 1674 AGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTG 1733
Qy 531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db 1734 GAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACT 1793
Qy 551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db 1794 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAAT 1853
Qy 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db 1854 GACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGG 1913
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Qy 611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db 1974 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033
Qy 631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db 2034 GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCA 2093
Qy 651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db 2094 GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACAGCC 2153
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Qy 691 ValAspMetAlaPheLeuGlyThrArgAla---+------------------------- 700
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Qy 701 ------------------GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
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Qy 774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLe 794

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Db       2514 GGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAAGCT 2573

Qy        794 uGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2574 GGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAGCACTGTGGATGGGCC 2633

Qy        814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPh 834
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2634 GTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGACAACAACGGGTT 2693

Qy        834 eIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2694 CATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTGC 2753

Qy        854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2754 TGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACTATGTATGACTATCA 2813

Qy        874 nAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuValSerProIl 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2814 GGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCCAAT 2873

Qy        894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGl 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2874 TTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCTGGA 2933

Qy        914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHi 934
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2934 GTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCATCA 2993

Qy        934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2994 CTCCCACAAACACAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGTGTT 3053

Qy        954 eValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLy 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3054 CGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCAGAA 3113

Qy        974 sValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspProTh 994
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3114 GGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCCCAC 3173

Qy        994 rCysAspCysSerIlePheProProVal 1003
              |||||||||||||||||||||||||||
Db       3174 CTGTGACTGCAGCATCTTCCCACCAGTG 3201
```

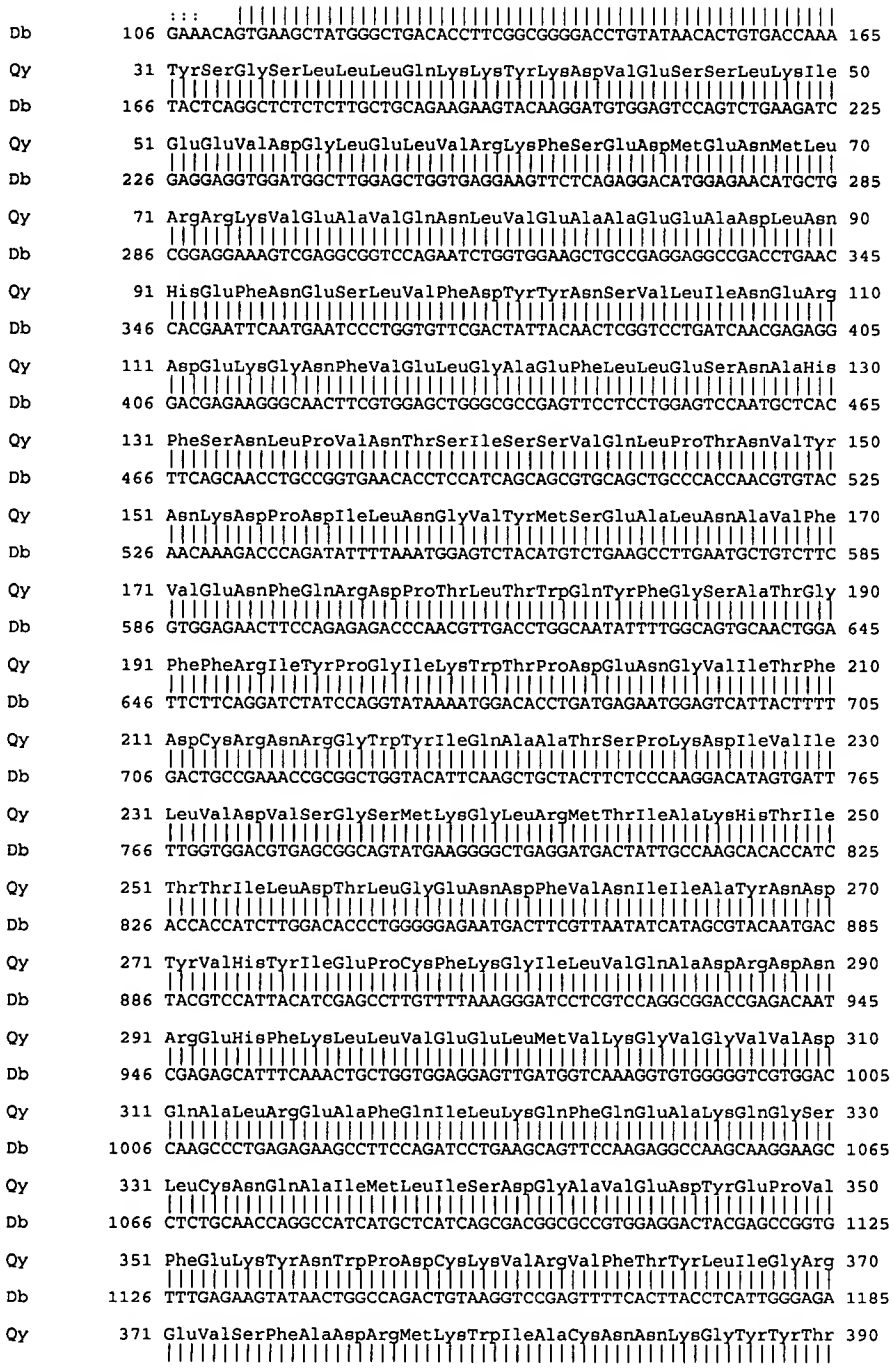
RESULT 14
ADN33188
ID ADN33188 standard; DNA; 3742 BP.
XX
AC ADN33188;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human transporter and ion channel (TRICH) gene SeqID73.
XX
KW transporters and ion channel; TRICH; neuroprotective; relaxant;
KW antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive;
KW antiinflammatory; thyromimetic; antiallergic; cerebroprotective;
KW gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;
KW antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;
KW virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;
KW nootropic; TRICH agonist; TRICH antagonist; gene therapy;
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
KW diabetes; Grave's disease; cancer; leukaemia; cervical cancer;
KW breast cancer; immunological disorder; scleroderma;
KW systemic lupus erythematosus; allergy; gastrointestinal disorder;
KW Crohn's disease; renal disorder; Goodpasture's syndrome; infection;
KW viral; bacterial; fungal; parasitic; protozoal; helminthic;
KW cardiovascular disorder; atherosclerosis; hepatic disease; cirrhosis;
KW transgenic animal; gene; ds; human.
XX
OS Homo sapiens.
XX
PN WO2004035755-A2.
XX
PD 29-APR-2004.
XX
PF 16-OCT-2003; 2003WO-US033087.
XX
PR 16-OCT-2002; 2002US-0419313P.
PR 23-OCT-2002; 2002US-0421033P.
PR 25-OCT-2002; 2002US-0421349P.
PR 04-NOV-2002; 2002US-0423516P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Hafalia AJA, Khare R, Lal PG, Yue H, Baughn MR, Thornton MB;
PI Lu DAM, Ison CH, Becha SD, Ding L, Warren BA, Lee SY, Swarnakar A;
PI Elliott VS, Richardson TW, Marquis JP, Ramkumar J, Murage J;
PI Raumann BE, Yao MG, Lu Y, Gietzen KJ, Yang YG, Chang H, Chawla NK;
PI Tran UK, Lee S, Yang J, Gandhi AR, Tribouley CM, Policky JL;
PI Ring HZ, Lee EA;
XX
DR WPI; 2004-348448/32.
DR P-PSDB; ADN33132.
XX
PT New TRICH polypeptides, useful for diagnosing, preventing, and treating
PT disorders associated with abnormal expression or activity of TRICH, e.g.
PT neuromuscular, immunological, cardiovascular disorders, cancer and/or
PT infections.
XX
PS Claim 5; SEQ ID NO 73; 285pp; English.
XX
CC This invention relates to novel human transporters and ion channel
CC (TRICH) proteins and the nucleotide sequences which encode them. The
CC invention may be useful for the production of compounds with a
CC neuroprotective, relaxant, antithyroid, antidiabetic, cytostatic,
CC dermatological, immunosuppressive, antiinflammatory, thyromimetic,
CC antiallergic, cerebroprotective, gastrointestinal, hepatotropic,
CC nephrotropic, anticonvulsant, antiparkinsonian, antibacterial,
CC antiparasitic, fungicide, protozoacide, virucide, uropathic,
CC antirheumatic, cardiant, cardiovascular, anti-HIV or nootropic activity
CC acting as TRICH agonists or antagonists. In addition the disclosed
CC sequences may be useful for gene therapy. The invention may be useful in
CC diagnosing, preventing, and treating disorders associated with an
CC abnormal expression or activity of TRICH, such as neurodegenerative
CC disorders (for example Parkinson's disease, Alzheimer's disease),
CC muscular disorders (for example myotonic dystrophy, catatonia), endocrine
CC disorders (for example diabetes, Grave's disease), cancers (for example
CC leukaemia, cervical or breast cancers), immunological disorders (for
CC example scleroderma, systemic lupus erythematosus, allergies),
CC gastrointestinal disorders (for example Crohn's disease), renal disorders
CC (for example Goodpasture's syndrome), infections (for example viral,
CC bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular
CC disorders (for example atherosclerosis), or hepatic diseases (for example
CC cirrhosis). TRICH or its fragments may also be used in screening for
CC compounds that specifically bind to and modulate the activity of TRICH.
CC The nucleotides can be used to create humanised animals or transgenic
CC animals to model human disease. The present sequence is that of a human
CC transporter and ion channel (TRICH) gene of the invention.
XX
SQ Sequence 3742 BP; 882 A; 1052 C; 1053 G; 755 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3742
Score:	5127.50	Matches:	998
Percent Similarity:	92.62%	Conservative:	6
Best Local Similarity:	92.07%	Mismatches:	31
Query Match:	89.55%	Indels:	51
DB:	13	Gaps:	2

US-09-833-222A-10 (1-1090) x ADN33188 (1-3742)

```
Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
```


Db 106 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 165
Qy 31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
Db 166 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 225
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
Db 226 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 285
Qy 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
Db 286 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 345
Qy 91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
Db 346 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGATCAACGAGAGG 405
Qy 111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
Db 406 GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCTCAC 465
Qy 131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
Db 466 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTGTAC 525
Qy 151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db 526 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 585
Qy 171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
Db 586 GTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACTGGA 645
Qy 191 PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
Db 646 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 705
Qy 211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
Db 706 GACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTGATT 765
Qy 231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db 766 TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACCATC 825
Qy 251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db 826 ACCACCATCTTGGACACCCTGGGGGAGAATGACTTCGTTAATATCATAGCGTACAATGAC 885
Qy 271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
Db 886 TACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGACAAT 945
Qy 291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
Db 946 CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTGGAC 1005
Qy 311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db 1006 CAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGAAGC 1065
Qy 331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db 1066 CTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCGGTG 1125
Qy 351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db 1126 TTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGGAGA 1185
Qy 371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db 1186 GAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTACACG 1245
Qy 391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
Db 1246 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1305
Qy 411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
Db 1306 CGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGACAGC 1365
Qy 431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
Db 1366 AAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGTTCACCACTGTGGCCATGCCAGTC 1425
Qy 451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db 1426 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCAGAT 1485
Qy 471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLys---------- 484
Db 1486 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGATGCCCAGCACAAACAGC 1545
Qy 485 ----------LeuGlyValHisGlyTyrAlaPheLe 493
Db 1546 AGGCCTAATGCGCCTCCACCCTGGACTCTGGCAGCTTGGAGTGCACGGATACGCCTTTCT 1605
Qy 493 uAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGluGl 513
Db 1606 GAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTGTACAGAGAGGG 1665
Qy 513 yLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGluTrpGl 533
Db 1666 GAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAAGTGGAGTGGGA 1725
Qy 533 uAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeuSerMe 553
Db 1726 AGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGTACTCTCTCGAT 1785
Qy 553 tAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAspTyrPh 573
Db 1786 GGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACCAATGACTACTT 1845
Qy 573 ePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHisGl 593
Db 1846 CTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCCCGGGGCCACGG 1905
Qy 593 yGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHisPr 613
Db 1906 AGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGACTTGCTTCACCC 1965
Qy 613 oAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisAr 633
Db 1966 AGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCAGACCACCG 2025
Qy 633 gLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeuGl 653
Db 2026 GAAGCTCGGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGACCCAGACCTGGA 2085
Qy 653 uCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMetGl 673
Db 2086 GTG---------- 2088
Qy 673 uAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAspMe 693
Db 2089 ----------GAGTCTGAACACGTGGTGGACAT 2111
Qy 693 tAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGluLy 713
Db 2112 GGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAA 2171
Qy 713 sValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspAr 733
Db 2172 GGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACCCTGGACCG 2231

```
Qy        733 gPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLe 753
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Db       2232 CTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTCGTCTTCAACCT 2291

Qy        753 uArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAl 773
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Db       2292 CCGCTGGGCAGAAGGACCAGAAAGTGCGGGTGAACCCATGGTGGTGACGGCAAGCACAGC 2351

Qy        773 aValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLy 793
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Db       2352 TGTGGCGGTGACCGTGGACAAGAGGACAGCCATTGCTGCAGCCGCGGGCGTCCAAATGAA 2411

Qy        793 sLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGl 813
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db       2412 GCTGGAATTCCTCCAGCGCAAATTCTGGGCGGCAACGCGGCAGTGCAACACTGTGGATGG 2471

Qy        813 yProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsnGl 833
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Db       2472 GCCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCATCGACAACAACGG 2531

Qy        833 yPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGl 853
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2532 GTTCATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGG 2591

Qy        853 yAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTy 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2592 TGCTGTCCTGACCCAGCTGCTCAGCATGGGGGTGTTCAGCCAAGTGACAATGTATGACTA 2651

Qy        873 rGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuValSerPr 893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2652 TCAGGCCATGTGCAAACCCTCGAGTCACCACCACAGTGCAGCCCAGCCCCTGGTCAGCCC 2711

Qy        893 oIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLe 913
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Db       2712 AATTTCTGCCTTCTTGACGGCGACCAGGTGGCTGCTGCAGGAGCTGGTGCTGTTCCTGCT 2771

Qy        913 uGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHi 933
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Db       2772 GGAGTGGAGTGTCTGGGGCTCCTGGTACGACAGAGGGGCCGAGGCCAAAAGTGTCTTCCA 2831

Qy        933 sHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProVa 953
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db       2832 TCACTCCCACAAACACGAGAAGCAGGACCCGCTGCAGCCCTGCGACACGGAGTACCCCGT 2891

Qy        953 lPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGl 973
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2892 GTTCGTGTACCAGCCGGCCATCCGGGAGGCCAACGGGATCGTGGAGTGCGGGCCCTGCCA 2951

Qy        973 nLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuLeuValThrAspPr 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2952 GAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTCCTCCTGGTGACAGACCC 3011

Qy        993 oThrCysAspCysSerIleProProValLeuGlnGluAlaThrGluValLysTyrAs 1013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3012 CACCTGTGACTGCAGCATCTTCCCACCAGTGCTGCAGGAGGCGACAGAAGTCAAATATAA 3071

Qy       1013 nAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgArgProAspSerCy 1033
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db       3072 TGCCTCTGTCAAATGTGACCGGATGCGCTCCCAGAAGCCCCGCCGGCGACCAGACTCCTG 3131

Qy       1033 sHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGlyPheSerSe 1053
              ||||||||||||||||||||          :::          |||   :::       |||::
Db       3132 CCACGCCTTCCATCCAGAGGAGAATGCCCAGGACTGCGGCGGCGCCTCGGACACCTCAGC 3191

Qy       1053 rProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGlyMetProMe 1073
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Db       3192 CTCGCCGCCCCTACTCCTGCT-GCCTGTGTGTGCCTGGGGGCTACTGCCCCAACTCCTGC 3250

Qy       1073 tAsnThrPro 1076
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Db       3251 GGTGACACCA 3260
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RESULT 15
AAD22004
ID   AAD22004 standard; cDNA; 4125 BP.
XX
AC   AAD22004;
XX
DT   12-FEB-2002  (first entry)
XX
DE   Human transporters and ion channels (TRICH)-12 cDNA.
XX
KW   Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis;
KW   diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia;
KW   cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia;
KW   neurological disorder; Alzheimer's disease; cataract; infertility;
KW   Wilson's disease; schizophrenia; Grave's disease; addison's disease;
KW   Huntington's disease; multiple sclerosis; meningitis; hypotensive;
KW   cardiant; nootropic; neuroprotective; neuroleptic; ophthalmological;
KW   antithyroid; anticonvulsant; goitre; antiinflammatory; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3933
FT                   /*tag=  a
FT                   /product= "Human transporters and ion channels (TRICH)-
FT                   12"
XX
PN   WO200177174-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-US011206.
XX
PR   06-APR-2000; 2000US-0195595P.
PR   12-APR-2000; 2000US-0196872P.
PR   20-APR-2000; 2000US-0199020P.
PR   28-APR-2000; 2000US-0200552P.
PR   05-MAY-2000; 2000US-0202348P.
PR   11-MAY-2000; 2000US-0203495P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Reddy R,  Thornton M,  Borowsky ML,  Tang YT,  Khan FA,  Tribouley CM;
PI   Gandhi AR,  Yao MG,  Sanjanwala MS,  Baughn MR,  Nguyen DB,  Policky JL;
PI   Yue H,  Seilhamer JJ,  Walia NK,  Lal P,  Kearney L,  Walsh RT,  Lu DAM;
PI   Lu Y,  Greene BD,  Raumann BE,  Patterson C;
XX
DR   WPI; 2002-017448/02.
DR   P-PSDB; AAE13285.
XX
PT   Polypeptides of human transporters and ion channels, useful for
PT   diagnosing, treating or preventing disorders of transport, neurological,
PT   muscle, immunological and cell proliferative disorders.
XX
PS   Claim 5; Page 147-148; 150pp; English.
XX
CC   The invention relates to human transporters and ion channels (TRICH) and
CC   the polynucleotides encoding them. The composition comprising TRICH or
CC   agonist of TRICH is useful for treating a disease or condition associated
CC   with decreased expression of functional TRICH or condition associated
CC   with overexpression of TRICH respectively. The composition comprising Ab
CC   is useful for diagnosing a condition of disease associated with
CC   expression of TRICH in a subject, where the disorders include a transport
CC   disorder such as akinesia, cystic fibrosis, diabetes mellitus,
CC   Parkinson's disease, myasthenia gravis, cardiac disorders associated with
CC   transport e.g. angina, hypertension, myocarditis, neurological disorders
CC   associated with transport e.g. Alzheimer's disease, Wilson's disease,
CC   schizophrenia, cataracts, infertility, hyperglycaemia, Grave's disease,
CC   goitre, addison's disease, Huntington's disease, dementia, multiple
CC   sclerosis, bacterial and viral meningitis. TRICH DNA is useful for
CC   generating a transcript image of a tissue or cell type, which represents
CC   the global pattern of gene expression by a particular tissue or cell type
CC   and for analysing the proteome of a tissue or cell type. TRICH DNA is
```

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CC   used in gene therapy. The present sequence is human TRICH12 cDNA
XX
SQ   Sequence 4125 BP; 989 A; 1109 C; 1188 G; 839 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0              Length:         4125
Score:                  3808.00        Matches:        750
Percent Similarity:     80.90%         Conservative:   4
Best Local Similarity:  80.47%         Mismatches:     14
Query Match:            66.50%         Indels:         164
DB:                     6              Gaps:           2

US-09-833-222A-10 (1-1090) x AAD22004 (1-4125)

Qy         11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
              :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 1179

Qy         31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 TACTCAGGCTCTCTCTTGCTGCAGAAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC 1239

Qy         51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG 1299

Qy         71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1300 CGGAGGAAAGTCGAGGCGGTCCAGAATCTGGTGGAAGCTGCCGAGGAGGCCGACCTGAAC 1359

Qy         91 HisGluPheAsnGluSerLeuVal---------------------------------- 98
              ||||||||||||||||||||||
Db       1360 CACGAATTCAATGAATCCCTGGTGGAACCTGGCGTGGGAGTTGGCGTGGGGATGTCCGTG 1419

Qy         98 ---------------------------------------------------------- 98

Db       1420 ACGCAGTCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGACGCAGTCCGGCGTGGGAGTT 1479

Qy         98 ---------------------------------------------------------- 98

Db       1480 GGCGTGGGGATGTCCATAACGCTGTCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGAGG 1539

Qy         98 ---------------------------------------------------------- 98

Db       1540 CAGTCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGACGCAGTCCGGCGTGGGAGTTGGC 1599

Qy         98 ---------------------------------------------------------- 98

Db       1600 GTGGGGATGTCCGTGACGCAGTCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGAGGCAG 1659

Qy         98 ---------------------------------------------------------- 98

Db       1660 TCCGGCGTGGGAGTTGGCGTGGGGATGTCCGTGACGCAGTCCTGGGGGGTGTTCAGTGCC 1719

Qy         98 ---------------------------------------------------------- 98

Db       1720 CAGCGCGCCGCCGCGGGTGCTTGTGTAGACTCTGATGGCCGCCCGGCCCCGGCCCTCTCG 1779

Qy         98 ---------------------------------------------------------- 98

Db       1780 TCCTCTCACCTGCGCCGTTTCTCTTCCTCTCTCCGCCTGTCCCGGTGCTCGGGCCGCC 1839

Qy         99 ----------------------------PheAspTyrTyrAsnSerValLeuIleAsnGlu 109
                                          ||||||||||||||||||||||||||||||||
Db       1840 TCCGTGGGCCTCACCCGTCCACCCCAGTTCGACTATTACAACTCGGTCCTGATCAACGAG 1899

Qy        110 ArgAspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAla 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1900 AGGGACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCGAGTTCCTCCTGGAGTCCAATGCT 1959

Qy        130 HisPheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnVal 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1960 CACTTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCACCAACGTG 2019

Qy        150 TyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaVal 169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2020 TACAACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTC 2079

Qy        170 PheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThr 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2080 TTCGTGGAGAACTTCCAGAGAGACCCAACGTTGACCTGGCAATATTTTGGCAGTGCAACT 2139

Qy        190 GlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThr 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2140 GGATTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACT 2199

Qy        210 PheAspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleVal 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2200 TTTGACTGCCGAAACCGCGGCTGGTACATTCAAGCTGCTACTTCTCCCAAGGACATAGTG 2259

Qy        230 IleLeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThr 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2260 ATTTTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCCAAGCACACC 2319

Qy        250 IleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsn 269
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db       2320 ATCACCACCATCTTGGACACCCTGGGGGAGAATGACTTCATTAATATCATAGCGTACAAT 2379

Qy        270 AspTyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAsp 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2380 GACTACGTCCATTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCCAGGCGGACCGAGAC 2439

Qy        290 AsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValVal 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2440 AATCGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAGGTGTGGGGGTCGTG 2499

Qy        310 AspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGly 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2500 GACCAAGCCCTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAAGAGGCCAAGCAAGGA 2559

Qy        330 SerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluPro 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2560 AGCCTCTGCAACCAGGCCATCATGCTCATCAGCGACGGCGCCGTGGAGGACTACGAGCCG 2619

Qy        350 ValPheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGly 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2620 GTGTTTGAGAAGTATAACTGGCCAGACTGTAAGGTCCGAGTTTTCACTTACCTCATTGGG 2679

Qy        370 ArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyr 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2680 AGAGAAGTGTCTTTTGCTGACCGCATGAAGTGGATTGCATGCAACAACAAAGGCTACTAC 2739

Qy        390 ThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeu 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2740 ACGCAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTC 2799

Qy        410 SerArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAsp 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2800 AGCCGCCCCATGGTCATCAACCACGACCACGACATCATCTGGACAGAGGCCTACATGGAC 2859

Qy        430 SerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetPro 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2860 AGCAAGCTCCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACTGTGGCCATGCCA 2919

Qy        450 ValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySer 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2920 GTCTTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTCTCCTGGGTGTGGTGGGCTCA 2979

Qy        470 AspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGly 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2980 GATGTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGA 3039

Qy        490 TyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3040 TACGCCTTTCTGAACACCAACAATGGCTACATCCTCTCCCATCCCGACCTCCGGCCCCTG 3099
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Qy        510 TyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGlu 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3100 TACAGAGAGGGGAAGAAACTAAAACCCAAACCTAACTACAACAGTGTGGATCTCTCCGAA 3159

Qy        530 ValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGly 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3160 GTGGAGTGGGAAGACCAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAAACAGGT 3219

Qy        550 ThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThr 569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3220 ACTCTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGCGAGTTCTTTTCCTGACC 3279

Qy        570 AsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSer 589
              ||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db       3280 AATGACTACTTCTTCACGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGCTGTCC 3339

Qy        590 ArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAsp 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3340 CGGGGCCACGGAGAATACATCCTTCTGGGGAACACGTCTGTGGAAGAAGGCCTGCATGAC 3399

Qy        610 LeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAsp 629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3400 TTGCTTCACCCAGACTTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGAC 3459

Qy        630 ProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAsp 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3460 CCAGACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCCTCACCAGGAAGGAC 3519

Qy        650 ProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThr 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3520 CCAGACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTGTTTGACGCGGTGGTGACA 3579

Qy        670 AlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHis 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3580 GCCCCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACAC 3639

Qy        690 ValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheVal 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3640 GTGGTGGACATGGCCTTCCTGGGCACCCGGGCTGGCCTCCTGAGAAGCAGCTTGTTCGTG 3699

Qy        710 GlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPhe 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3700 GGCTCCGAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTC 3759

Qy        730 ThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3760 ACCCTGGACCGCTTCCCGCTGTGGTACCGCCAGGCCTCAGAGCATCCTGCTGGCAGCTTC 3819

Qy        750 ValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThr 769
              ||||||||||||||||||||||||||||          |||   |||
Db       3820 GTCTTCAACCTCCGCTGGGCAGAAGGACCA---------GGACGCCCTTCTGCCAAAGGC 3870

Qy        770 AlaSerThrAlaValAlaValThrValAspLysArg 781
                      :::      |||:::   ||||||
Db       3871 CTTCCACCACCACTTTGCCAAACCATCCTCAAGCGT 3906
```

Search completed: November 17, 2005, 00:11:21
Job time : 1525 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 16, 2005, 03:09:42 ; Search time 171 Seconds
(without alignments)
2465.315 Million cell updates/sec

Title: US-09-833-222A-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTPVPVLLGGNIRVYAL 1090

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5726	100.0	1090	6	ABP59509	Abp59509 Human vol
2	5726	100.0	1090	7	ADF71820	Adf71820 Human cal
3	5386.5	94.1	1120	3	AAY92321	Aay92321 Human alp
4	5385.5	94.1	1207	7	ADE08021	Novel pro
5	5363	93.7	1097	4	AAU01038	Aau01038 Human sec
6	5363	93.7	1097	4	AAB62262	Aab62262 Human cal
7	5276	92.1	1069	4	AAU01037	Aau01037 Human sec
8	5276	92.1	1069	4	AAB62261	Aab62261 Human cal
9	5244.5	91.6	1096	3	AAY92324	Aay92324 Human alp
10	5234.5	91.4	1075	5	AAU09869	Aau09869 Novel hum
11	5230.5	91.3	1114	5	AAU09870	Aau09870 Novel hum
12	5179	90.4	1050	4	AAU01036	Aau01036 Human sec
13	5179	90.4	1050	4	AAB62260	Aab62260 Human cal
14	4649	81.2	1096	3	AAY92323	Aay92323 Human alp
15	3808	66.5	1310	5	AAE13285	Aae13285 Human tra
16	3422	59.8	1091	5	AAE16666	Aae16666 Mouse cal
17	3419.5	59.7	1077	4	AAU01026	Aau01026 Mouse wil
18	3419.5	59.7	1077	4	AAB62250	Aab62250 Human cal
19	3416.5	59.7	1091	5	AAE16665	Aae16665 Human cal
20	3410.5	59.6	1065	4	AAU01019	Aau01019 Human sec
21	3410.5	59.6	1085	3	AAY92320	Aay92320 Human alp
22	3410.5	59.6	1085	4	AAU01024	Aau01024 Human sec
23	3410.5	59.6	1085	4	AAB62248	Aab62248 Human cal
24	3400.5	59.4	1071	4	AAB62243	Aab62243 Human cal
25	3326.5	58.1	1038	4	AAU01018	Aau01018 Human sec
26	3326.5	58.1	1038	4	AAB62242	Aab62242 Human cal
27	3278.5	57.3	1019	4	AAU01017	Aau01017 Human sec
28	3278.5	57.3	1019	4	AAB62241	Aab62241 Human cal
29	3029.5	52.9	947	6	ABB99658	Abb99658 Amino aci
30	2449	42.8	562	8	ADN33132	Adn33132 Human tra
31	2306	40.3	497	7	ADK40916	Adk40916 Novel hum
32	2306	40.3	497	8	ADR15609	Adr15609 Kinase 41
33	1870.5	32.7	519	3	AAY70460	Aay70460 Human mem
34	1792.5	31.3	350	4	AAU01022	Aau01022 Human sec
35	1792.5	31.3	350	4	AAB62246	Aab62246 Human cal
36	1695	29.6	323	4	AAU01021	Aau01021 Human sec
37	1695	29.6	323	4	AAB62245	Aab62245 Human cal
38	1598	27.9	304	4	AAU01020	Aau01020 Human sec
39	1598	27.9	304	4	AAB62244	Aab62244 Human cal
40	1565	27.3	1258	8	ADO16905	Ado16905 Tobacco b
41	1554.5	27.1	1271	8	ADO16903	Ado16903 Tobacco b
42	1497.5	26.2	1215	4	AAE02340	Aae02340 D. melano
43	1410	24.6	2172	4	ABB67958	Abb67958 Drosophil
44	1392.5	24.3	1245	8	ADO16901	Ado16901 Tobacco b
45	1322.5	23.1	1022	4	ABB62234	Abb62234 Drosophil

ALIGNMENTS

RESULT 1
ABP59509
ID ABP59509 standard; protein; 1090 AA.
XX
AC ABP59509;
XX
DT 03-MAR-2003 (first entry)
XX
DE Human voltage gated calcium channel alpha2delta-4 subunit.
XX
KW Human; voltage gated calcium channel; alpha2delta-4 subunit;
KW antiparkinsonian; tranquilizer; neuroprotective; anticonvulsant;
KW antimigraine; analgesic; cytostatic; antidepressant; antiinflammatory;
KW gene therapy; epilepsy; migraine; ataxia; vestibular defect;
KW chronic pain; neuropathic pain; Parkinson's disease; depression; cancer;
KW inflammation; seizure-related syndrome; anxiety; multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO200283847-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011297.
XX
PR 11-APR-2001; 2001US-00833222.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Qin N, Codd E;
XX
DR WPI; 2003-093006/08.
DR N-PSDB; ABZ20598.
XX
PT New nucleic acid molecule encoding human alpha2 delta4 calcium channel
PT subunit protein, useful for diagnosing and treating a disease associated
PT with defects in the subunit protein, e.g. epilepsy, migraine, ataxia or
PT chronic pain.
XX
PS Claim 13; Page 56-59; 91pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC voltage gated calcium channel alpha2delta-4 subunit. The sequences are
CC useful for diagnosing and treating a disease or disorder associated with
CC a defective alpha2delta-4 subunit, such as seizure-related syndromes,
CC epilepsy, migraine, ataxia, vestibular defects, chronic pain, neuropathic
CC pain, mood, sleep interference, anxiety, ALS, multiple sclerosis, mania,
CC Parkinson's disease, substance abuse/addiction syndromes, depression,

```
CC   cancer, or inflammation. The present sequence is the protein of the
CC   invention
XX
SQ   Sequence 1090 AA;

  Query Match           100.0%;  Score 5726;  DB 6;  Length 1090;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1090;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAVALGTRRRDRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAVALGTRRRDRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVR 60

Qy         61 KFSEDMENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KFSEDMENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELG 120

Qy        121 AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTL 180

Qy        181 TWQYFGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TWQYFGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKG 240

Qy        241 LRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEE 300

Qy        301 LMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCK 360

Qy        361 VRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHD 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHD 420

Qy        421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLA 480

Qy        481 PRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLR 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLR 540

Qy        541 TAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGN 600

Qy        601 TSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVR 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVR 660

Qy        661 EVLFDAVVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFL 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EVLFDAVVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFL 720

Qy        721 TPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDK 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TPEDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDK 780

Qy        781 RTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKR 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 RTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKR 840

Qy        841 SRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 SRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTA 900

Qy        901 TRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAI 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAI 960

Qy        961 REANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDR 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 REANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDR 1020

Qy       1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRQEHIGMPMNTPVPVL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRQEHIGMPMNTPVPVL 1080

Qy       1081 LGGNIRVYAL 1090
              ||||||||||
Db       1081 LGGNIRVYAL 1090


RESULT 2
ADF71820
ID   ADF71820 standard; protein; 1090 AA.
XX
AC   ADF71820;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human calcium channel alpha2delta4 subunit.
XX
KW   neuroprotective; cytostatic; gene therapy; calcium channel;
KW   alpha2delta-4; amyotrophic lateral sclerosis; multiple sclerosis; cancer;
KW   human.
XX
OS   Homo sapiens.
XX
PN   US2003170785-A1.
XX
PD   11-SEP-2003.
XX
PF   10-APR-2002; 2002US-00119624.
XX
PR   11-APR-2001; 2001US-00833222.
XX
PA   (QINN/) QIN N.
PA   (CODD/) CODD E.
XX
PI   Qin N,  Codd E;
XX
DR   WPI; 2003-898262/82.
DR   N-PSDB; ADF71819.
XX
PT   New human alpha2 delta4 calcium channel subunit protein and nucleic acid
PT   molecule, useful for diagnosing and treating diseases associated with
PT   defective calcium channel subunit, e.g. cancer and multiple sclerosis.
XX
PS   Claim 17; SEQ ID NO 10; 37pp; English.
XX
CC   The invention describes a new isolated and purified nucleic acid molecule
CC   comprising: a sequence having at least a 70% identity to nucleotides 1-
CC   224 or 3308-3486 of a sequence of 3486 bp (S1) fully defined in the
CC   specification; at least 15 sequential bases of the polynucleotide of (a);
CC   or a sequence that is complementary to the polynucleotide of (a) or (b).
CC   Specifically claimed is an alpha2delta-4 nucleic acid molecule comprising
CC   a sequence of 3486 bp fully defined in the specification and encoding an
CC   alpha2delta-4 calcium channel subunit protein having a sequence of 1090
CC   amino acids fully defined in the specification. The nucleic acid molecule
CC   and polypeptide are useful in diagnosing and treating a disease or
CC   disorder associated with a defective alpha2delta-4 subunit, such as
CC   amyotrophic lateral sclerosis, multiple sclerosis or cancer. The methods
CC   may be used for identifying compounds capable of treating the above-
CC   mentioned diseases or disorders. This is the amino acid sequence of human
CC   calcium channel alpha2delta-4 subunit.
XX
SQ   Sequence 1090 AA;

  Query Match           100.0%;  Score 5726;  DB 7;  Length 1090;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1090;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MAVALGTRRRDRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAVALGTRRRDRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVR 60

Qy         61 KFSEDMENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KFSEDMENMLRRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELG 120

Qy        121 AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTL 180

Qy        181 TWQYFGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TWQYFGSATGFFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKG 240

Qy        241 LRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LRMTIAKHTITTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEE 300

Qy        301 LMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LMVKGVGVVDQALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCK 360

Qy        361 VRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHD 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VRVFTYLIGREVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHD 420

Qy        421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLA 480

Qy        481 PRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLR 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 PRYKLGVHGYAFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLR 540

Qy        541 TAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGN 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAMINRETGTLSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGN 600

Qy        601 TSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVR 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TSVEEGLHDLLHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVR 660

Qy        661 EVLFDAVVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFL 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 EVLFDAVVTAPMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFL 720

Qy        721 TPEDEASVFTLDRFPLWYRQASEHPAGSFVPNLRWAEGPESAGEPMVVTASTAVAVTVDK 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TPEDEASVFTLDRFPLWYRQASEHPAGSFVPNLRWAEGPESAGEPMVVTASTAVAVTVDK 780

Qy        781 RTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKR 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 RTAIAAAAGVQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKR 840

Qy        841 SRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 SRETGRFLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTA 900

Qy        901 TRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAI 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TRWLLQELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAI 960

Qy        961 REANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDR 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 REANGIVECGPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDR 1020

Qy       1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRQEHIGMPMNTPVPVL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRQEHIGMPMNTPVPVL 1080

Qy       1081 LGGNIRVYAL 1090
              ||||||||||
Db       1081 LGGNIRVYAL 1090
```

RESULT 3
AAY92321
ID AAY92321 standard; protein; 1120 AA.
XX
AC AAY92321;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human alpha-2-delta-D calcium channel subunit.
XX
KW alpha-2-delta-D; calcium channel subunit; 3p21.1; gabapentin; cytostatic;
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant.
XX
OS Homo sapiens.
XX
PN WO200020450-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US023519.
XX
PR 07-OCT-1998; 98US-0103322P.
PR 30-OCT-1998; 98US-0106473P.
PR 29-DEC-1998; 98US-0114088P.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Johns MA, Moldover B, Offord JD;
XX
DR WPI; 2000-303744/26.
DR N-PSDB; AAA09254.
XX
PT New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT anxiety, multiple sclerosis or cancer.
XX
PS Claim 8; Page 67; 88pp; English.
XX
CC The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 12p13.1. This gene and the related
CC alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
CC related syndromes, migraine, ataxia, vestibular defects, chronic pain,
CC sleep interference, anxiety, amyotropic lateral sclerosis (ALS), multiple
CC sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
CC syndromes, mood, depression or cancer
XX
SQ Sequence 1120 AA;

Query Match 94.1%; Score 5386.5; DB 3; Length 1120;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1033; Conservative 5; Mismatches 13; Indels 3; Gaps 2;

```
Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237
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Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 777

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 837

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        838 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 897

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 957

Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 1017

Qy        971 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1077

Qy       1031 DSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
              ||||||||   : | | |  :| :|  | | :|
Db       1078 DSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1110


RESULT 4
ADE08021
ID   ADE08021 standard; protein; 1207 AA.
XX
AC   ADE08021;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Novel protein (useful for identifying genetic disorders) #176.
XX
KW   novel gene; novel protein; tissue marker; molecular weight marker;
KW   chromosome marker; genetic disorder.
XX
OS   Unidentified.
XX
PN   WO2003054152-A2.
XX
PD   03-JUL-2003.
XX
PF   10-DEC-2002; 2002WO-US039555.
XX
PR   10-DEC-2001; 2001US-0339739P.
PR   11-DEC-2001; 2001US-0339453P.
PR   14-MAR-2002; 2002US-0365091P.
PR   14-MAR-2002; 2002US-0365384P.
PR   12-APR-2002; 2002US-0372381P.
PR   12-APR-2002; 2002US-0372615P.
PR   22-APR-2002; 2002US-00128558.
PR   24-APR-2002; 2002US-0376045P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Asundi V,  Goodrich RW,  Ren F,  Zhang J,  Zhao QA,  Wang J;
PI   Ghosh M,  Xue AJ,  Wehrman T,  Weng G,  Zhou P,  Drmanac RT,  Wang Z;
PI   Ma Y,  Wang D,  Chen R,  Xu C,  Boyle BJ;
XX
DR   WPI; 2003-569235/53.
DR   N-PSDB; ADE07110.
XX
PT   New polynucleotides, useful for expressing recombinant proteins for
PT   analysis, characterization or therapeutic use, or as markers for tissues
PT   in which the corresponding protein is preferentially expressed.
XX
PS   Claim 20; SEQ ID NO 1087; 1177pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of novel
CC   proteins. The DNA and protein sequences of the invention are useful as:
CC   markers for tissues in which the corresponding protein is preferentially
CC   expressed; as molecular weight markers on gels; as chromosome markers or
CC   tags; to identify chromosomes or to map related gene positions; and to
CC   compare with endogenous DNA sequences in patients to identify potential
CC   genetic disorders. The present amino acid sequence represents a protein
CC   of the invention.
XX
SQ   Sequence 1207 AA;

  Query Match             94.1%;  Score 5385.5;  DB 7;  Length 1207;
  Best Local Similarity   97.9%;  Pred. No. 0;
  Matches 1032;  Conservative    6;  Mismatches   13;  Indels    3;  Gaps    2;

Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 204

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 264

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 324

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 384

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 TTILDTLGENDFINIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 444

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 504

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 564

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 624

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 684

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 744

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 804

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 864

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 924

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
                ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        925 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 984

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 1044

Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1045 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 1104

Qy        971 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1030
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1164

Qy       1031 DSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
                |||||||||   : | | |  :| :|  | | :|
Db       1165 DSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1197


RESULT 5
AAU01038
ID   AAU01038 standard; protein; 1097 AA.
XX
AC   AAU01038;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Human secreted soluble alpha2delta calcium channel subunit #18 protein.
XX
KW   Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW   alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW   gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW   filter binding assay; wheat germ lectin flashplate assay.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 747. .749
FT                   /note= "Encoded by GCTGGC"
FT   Misc-difference 763. .764
FT                   /note= "Encoded by TCCGAGTGGCCTCCTGAGAAGCAG
FT                   CTTGTTCGTGGGCTCCGAGAAGGTCTCCGAC"
XX
PN   WO200119870-A2.
XX
PD   22-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-EP009137.
XX
PR   16-SEP-1999;   99US-00397550.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Brown JP,  Bertelli F;
XX
DR   WPI; 2001-235262/24.
DR   N-PSDB; AAS01433.
XX
PT   Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT   Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT   Wheat Germ Lectin Flashplate assays.
XX
PS   Claim 27; Page 156-160; 160pp; English.
XX
CC   The present sequence represents human secreted calcium channel
CC   alpha2delta subunit #18 which is soluble and retains the functional
CC   characteristics of the full length or wild type alpha2delta subunit
CC   (AAU01025) from which it is derived. The invention relates to truncated
CC   alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC   which retain their affinity for radioactively labelled gabapentin. The
CC   alpha2delta subunit is 1 of the components of the heteromultimeric
CC   voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC   and non-neuronal tissues including heart and skeletal muscle. Numerous
CC   soluble forms of the human calcium channel alpha2delta subunits (AAU01014
CC   -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
CC   calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
CC   The secreted soluble alpha2delta subunit may be used in assays e.g.
CC   scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC   filter binding or wheat germ lectin flashplate assays to detect or
CC   measure the binding or interaction of a ligand (e.g. gabapentin, L-
CC   Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
CC   Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
CC   subunit
XX
SQ   Sequence 1097 AA;

  Query Match             93.7%;  Score 5363;  DB 4;  Length 1097;
  Best Local Similarity   98.8%;  Pred. No. 0;
  Matches 1028;  Conservative    2;  Mismatches    8;  Indels    2;  Gaps    2;

Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
                : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477
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Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRA-GLLRSSLFVGSEKVSDRKFLTPEDEASVF 729
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        718 PMEAYWTALALNMSEESEHVVDMAFLGTRASGLLRSSLFVGSEKVSDRKFLTPEDEASVF 777

Qy        730 TLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAG 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 TLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAG 837

Qy        790 VQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLG 849
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        838 VQMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLG 897

Qy        850 EVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELV 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 EVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELV 957

Qy        910 LFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVEC 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 LFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVEC 1017

Qy        970 GPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRR 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRR 1077

Qy       1030 PDSCHAFHPEVRVEADRGWA 1049
              |||||||||   : | | |
Db       1078 PDSCHAFHPEENAQ-DCGGA 1096
```

RESULT 6
AAB62262
ID AAB62262 standard; protein; 1097 AA.
XX
AC AAB62262;
XX
DT 11-JUN-2001 (first entry)
XX
DE Human calcium channel alpha2delta subunit.
XX
KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human.
XX
OS Homo sapiens.
XX
PN WO200120336-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP009136.
XX
PR 16-SEP-1999; 99US-00397549.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
XX
DR WPI; 2001-257902/26.
XX
PT Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
PT the ligands identified are useful for treating disorders of the nervous
PT system, including pain.
XX
PS Disclosure; Page 154-157; 158pp; English.
XX
CC The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alpha2delta subunit
XX
SQ Sequence 1097 AA;

Query Match 93.7%; Score 5363; DB 4; Length 1097;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1028; Conservative 2; Mismatches 8; Indels 2; Gaps 2;

```
Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717
```

```
Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRA-GLLRSSLFVGSEKVSDRKFLTPEDEASVF 729
              ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        718 PMEAYWTALALNMSEESEHVVDMAFLGTRASGLLRSSLFVGSEKVSDRKFLTPEDEASVF 777

Qy        730 TLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAG 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 TLDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAG 837

Qy        790 VQMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLG 849
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        838 VQMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLG 897

Qy        850 EVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELV 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 EVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELV 957

Qy        910 LFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVEC 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 LFLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVEC 1017

Qy        970 GPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRR 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GPCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRR 1077

Qy       1030 PDSCHAFHPEVRVEADRGWA 1049
              |||||||||   : | | |
Db       1078 PDSCHAFHPEENAQ-DCGGA 1096
```

RESULT 7
AAU01037

ID AAU01037 standard; protein; 1069 AA.
XX
AC AAU01037;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #17 protein.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay.
XX
OS Homo sapiens.
XX
PN WO200119870-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP009137.
XX
PR 16-SEP-1999; 99US-00397550.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Brown JP, Bertelli F;
XX
DR WPI; 2001-235262/24.
DR N-PSDB; AAS01432.
XX
PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays.
XX
PS Claim 28; Page 153-156; 160pp; English.
XX
CC The present sequence represents human secreted calcium channel
CC alpha2delta subunit #17 which is soluble and retains the functional
CC characteristics of the full length or wild type alpha2delta subunit
CC (AAU01025) from which it is derived. The invention relates to truncated
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC which retain their affinity for radioactively labelled gabapentin. The
CC alpha2delta subunit is 1 of the components of the heteromultimeric
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits (AAU01014
CC -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
CC calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
CC The secreted soluble alpha2delta subunit may be used in assays e.g.
CC scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin, L-
CC Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
CC Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
CC subunit.
XX
SQ Sequence 1069 AA;

Query Match 92.1%; Score 5276; DB 4; Length 1069;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1008; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 777

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 837

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
```

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                ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        838 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 897

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 957

Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 1017

Qy        971 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMR 1022
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMR 1069


RESULT 8
AAB62261
ID   AAB62261 standard; protein; 1069 AA.
XX
AC   AAB62261;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Human calcium channel alpha2delta subunit.
XX
KW   Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW   nervous system disorder; pain; epilepsy; anxiety; human.
XX
OS   Homo sapiens.
XX
PN   WO200120336-A2.
XX
PD   22-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-EP009136.
XX
PR   16-SEP-1999;   99US-00397549.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bertelli F,  Brown JP,  Dissanayake V,  Suman-Chauhan N,  Gee NS;
XX
DR   WPI; 2001-257902/26.
DR   N-PSDB; AAF57569.
XX
PT   Competitive binding assay for screening ligands which bind a cerebral
PT   cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
PT   the ligands identified are useful for treating disorders of the nervous
PT   system, including pain.
XX
PS   Disclosure; Page 151-154; 158pp; English.
XX
CC   The invention relates to a new method for screening ligands which bind a
CC   cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC   preferably alpha2delta-1 subunit. The method comprises contacting a
CC   secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC   interest and a labelled compound which binds the subunit, followed by
CC   measuring the level of binding of the labelled compound to alpha2delta-1
CC   subunit. The method is useful for screening ligands, preferably
CC   biologically active products that modulate a nervous system function,
CC   which bind a cerebral cortical voltage-dependent calcium channel
CC   alpha2delta-1 subunit. The ligands identified by the method are useful
CC   for treating disorders of the nervous system, including pain, epilepsy
CC   and anxiety. The present sequence represents a human calcium channel
CC   alpha2delta subunit
XX
SQ   Sequence 1069 AA;

  Query Match           92.1%;  Score 5276;  DB 4;  Length 1069;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1008;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
               : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
               |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPPSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 777

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 837

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
               ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        838 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 897

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 957

Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 1017

Qy        971 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMR 1022
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMR 1069


RESULT 9
AAY92324
ID   AAY92324 standard; protein; 1096 AA.
XX
```

```
AC   AAY92324;
XX
DT   10-AUG-2000  (first entry)
XX
DE   Human alpha-2-delta-D polypeptide from splice variant 1.
XX
KW   alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
KW   anticonvulsant; antimigrane; antiparkinsonian; antidepressant;
KW   splice variant.
XX
OS   Homo sapiens.
XX
PN   WO200020450-A2.
XX
PD   13-APR-2000.
XX
PF   07-OCT-1999;   99WO-US023519.
XX
PR   07-OCT-1998;   98US-0103322P.
PR   30-OCT-1998;   98US-0106473P.
PR   29-DEC-1998;   98US-0114088P.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Johns MA,  Moldover B,  Offord JD;
XX
DR   WPI; 2000-303744/26.
DR   N-PSDB; AAA09729.
XX
PT   New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT   proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT   anxiety, multiple sclerosis or cancer.
XX
PS   Example 3; Page 73; 88pp; English.
XX
CC   This alpha-2-delta-D polypeptide is encoded by a splice variant that
CC   contains a 72 bp deletion of an internal exon. However, this sequence
CC   does not appear to have been reproduced in full in the specification (see
CC   AAA09729). The gene encodes a calcium channel subunit polypeptide. The
CC   gene has been mapped to chromosome 12p13.1. This gene and the related
CC   alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC   from abnormal calcium flux by introducing expression vectors containing
CC   the respective gene into mammalian cells. The antisense genes are also
CC   useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC   is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC   Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
CC   related syndromes, migraine, ataxia, vestibular defects, chronic pain,
CC   sleep interference, anxiety, amyotropic lateral sclerosis (ALS), multiple
CC   sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
CC   syndromes, mood, depression or cancer
XX
SQ   Sequence 1096 AA;

  Query Match             91.6%;  Score 5244.5;  DB 3;  Length 1096;
  Best Local Similarity   95.7%;  Pred. No. 0;
  Matches 1009;  Conservative    5;  Mismatches   13;  Indels   27;  Gaps    3;

Qy          11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
               : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy          71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy         131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy         191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy         251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         298 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy         311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy         371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy         431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy         491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||          
Db         538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAES---------- 585

Qy         551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
                                   |||||||||||||||||||||||| ||||||||||||||||||||||||
Db         586 -----------KRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 633

Qy         611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         634 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 693

Qy         671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         694 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 753

Qy         731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         754 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 813

Qy         791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
               |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         814 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 873

Qy         851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         874 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 933

Qy         911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         934 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 993

Qy         971 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1030
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         994 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1053

Qy        1031 DSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
               |||||||||   : | | |  :| :|  | | :|
Db        1054 DSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1086


RESULT 10
AAU09869
ID   AAU09869 standard; protein; 1075 AA.
XX
AC   AAU09869;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Novel human secreted protein #10.
XX
KW   Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine;
KW   antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human;
KW   cancer; autoimmune disease; wound healing disorder; infection;
KW   haematopoietic disorder; inflammatory disorder; infertility;
KW   neurological disease; psychiatric disease; cardiovascular disease;
KW   respiratory disease; renal; gastrointestinal.
```

```
XX
OS   Homo sapiens.
XX
PN   WO200179454-A1.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US011797.
XX
PR   13-APR-2000; 2000US-0196603P.
PR   24-APR-2000; 2000US-0199417P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Agarwal P,  Murdoch PR,  Rizvi SK,  Smith RF,  Xiang Z;
XX
DR   WPI; 2002-061975/08.
DR   N-PSDB; AAS17581.
XX
PT   New secreted proteins or polypeptides, useful for treating e.g. cancer,
PT   autoimmune diseases, wound healing disorder, infections, hematopoietic
PT   disorders, inflammatory disorders, infertility, cancer.
XX
PS   Claim 1; Page 67-70; 92pp; English.
XX
CC   The invention relates to an isolated novel secreted polypeptide (I) and
CC   polynucleotide (II). (I) and (II) are useful for treating cancer,
CC   autoimmune diseases, wound healing disorder, infections, haematopoietic
CC   disorders, inflammatory disorders, infertility, neurological and
CC   psychiatric diseases, cardiovascular diseases, respiratory diseases,
CC   renal diseases, or gastrointestinal diseases. These may also be used to
CC   treat diseases, abnormalities and disorders caused by abnormal
CC   expression, production, function and/or metabolism of the genes, as
CC   vaccines for inducing immunological response in a mammal, and in
CC   screening methods for detecting the effect of added compounds on the
CC   production of mRNA and polypeptide in cells. The polypeptides can be used
CC   as immunogens to produce antibodies immunospecific for the polypeptides,
CC   and to identify membrane-bound or soluble receptors. The polynucleotides
CC   may be used as diagnostic reagents, in chromosome localisation studies,
CC   and in tissue expression studies. The present sequence represents the
CC   amino acid sequence of novel human secreted protein #10
XX
SQ   Sequence 1075 AA;

  Query Match             91.4%;  Score 5234.5;  DB 5;  Length 1075;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 1011;  Conservative    7;  Mismatches   25;  Indels   11;  Gaps    4;

Qy         12 RVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLR 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 RVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENMLR 79

Qy         72 RKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHF 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 RKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAHF 139

Qy        132 SNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGF 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGF 199

Qy        192 FRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTIT 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 FRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTIT 259

Qy        252 TILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQ 311
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 TILDTLGENDFINIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQ 319

Qy        312 ALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGRE 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 ALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGRE 379

Qy        372 VSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSK 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 VSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSK 439

Qy        432 LLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYA 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 LLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYA 499

Qy        492 FLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTL 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 FLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTL 559

Qy        552 SMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLL 611
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        560 SMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDLL 619

Qy        612 HPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAP 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 HPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAP 679

Qy        672 MEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTL 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 MEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTL 739

Qy        732 DRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQ 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 DRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQ 799

Qy        792 MKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEV 851
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        800 MKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGEV 859

Qy        852 DGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLF 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 DGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLF 919

Qy        912 LLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECGP 971
              |||||||||||||||||       |||||||||||||||||||||||||||||||||||||
Db        920 LLEWSVWGSWYDRGAEA-------HKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECGP 972

Qy        972 CQKVFVVQQIPNSNLLLLVTDPT-CDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRRP 1030
              |||||||||||||||||||||| |     | :|       :|||||||||||||||||||
Db        973 CQKVFVVQQIPNSNLLLLVTDPTFCRMGSGPEILTLTVASAHNASVKCDRMRSQKLRRRP 1032

Qy       1031 DSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
              |||||||||   : | | |  :| :|  | | :|
Db       1033 DSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1065


RESULT 11
AAU09870
ID   AAU09870 standard; protein; 1114 AA.
XX
AC   AAU09870;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Novel human secreted protein #11.
XX
KW   Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine;
KW   antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human;
KW   cancer; autoimmune disease; wound healing disorder; infection;
KW   haematopoietic disorder; inflammatory disorder; infertility;
KW   neurological disease; psychiatric disease; cardiovascular disease;
KW   respiratory disease; renal; gastrointestinal.
XX
OS   Homo sapiens.
XX
PN   WO200179454-A1.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US011797.
```

```
XX
PR   13-APR-2000; 2000US-0196603P.
PR   24-APR-2000; 2000US-0199417P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Agarwal P,  Murdoch PR,  Rizvi SK,  Smith RF,  Xiang Z;
XX
DR   WPI; 2002-061975/08.
DR   N-PSDB; AAS17582.
XX
PT   New secreted proteins or polypeptides, useful for treating e.g. cancer,
PT   autoimmune diseases, wound healing disorder, infections, hematopoietic
PT   disorders, inflammatory disorders, infertility, cancer.
XX
PS   Claim 1; Page 70-73; 92pp; English.
XX
CC   The invention relates to an isolated novel secreted polypeptide (I) and
CC   polynucleotide (II). (I) and (II) are useful for treating cancer,
CC   autoimmune diseases, wound healing disorder, infections, haematopoietic
CC   disorders, inflammatory disorders, infertility, neurological and
CC   psychiatric diseases, cardiovascular diseases, respiratory diseases,
CC   renal diseases, or gastrointestinal diseases. These may also be used to
CC   treat diseases, abnormalities and disorders caused by abnormal
CC   expression, production, function and/or metabolism of the genes, as
CC   vaccines for inducing immunological response in a mammal, and in
CC   screening methods for detecting the effect of added compounds on the
CC   production of mRNA and polypeptide in cells. The polypeptides can be used
CC   as immunogens to produce antibodies immunospecific for the polypeptides,
CC   and to identify membrane-bound or soluble receptors. The polynucleotides
CC   may be used as diagnostic reagents, in chromosome localisation studies,
CC   and in tissue expression studies. The present sequence represents the
CC   amino acid sequence of novel human secreted protein #11
XX
SQ   Sequence 1114 AA;

  Query Match             91.3%;  Score 5230.5;  DB 5;  Length 1114;
  Best Local Similarity   95.7%;  Pred. No. 0;
  Matches 1010;  Conservative    8;  Mismatches   26;  Indels   11;  Gaps    4;

Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTILDTLGENDFINIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 777

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 837

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        838 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 897

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 957

Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
              |||||||||||||||||       ||||||||||||||||||||||||||||||||||||
Db        958 FLLEWSVWGSWYDRGAEA-------HKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 1010

Qy        971 PCQKVFVVQQIPNSNLLLLVTDPT-CDCSIFPPVLQEATEVKYNASVKCDRMRSQKLRRR 1029
              |||||||||||||||||||||||| |    | :|       :|||||||||||||||||
Db       1011 PCQKVFVVQQIPNSNLLLLVTDPTFCRMGSGPEILTLTVASAHNASVKCDRMRSQKLRRR 1070

Qy       1030 PDSCHAFHPEVRVEADRGWAGFSSPNP--LCLGLC 1062
              |||||||||   : | | |  :| :|  | | :|
Db       1071 PDSCHAFHPEENAQ-DCGGASDTSASPPLLLLPVC 1104


RESULT 12
AAU01036
ID   AAU01036 standard; protein; 1050 AA.
XX
AC   AAU01036;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Human secreted soluble alpha2delta calcium channel subunit #16 protein.
XX
KW   Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW   alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW   gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW   filter binding assay; wheat germ lectin flashplate assay.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 762. .763
FT                   /note= "Encoded by TCCGAGTGGCCTCCTGAGAAGCAG
FT                   CTTGTTCGTGGGCTCCGAGAAGGTCTCCGAC"
XX
PN   WO200119870-A2.
XX
PD   22-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-EP009137.
XX
PR   16-SEP-1999;   99US-00397550.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
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PI   Brown JP,  Bertelli F;
XX
DR   WPI; 2001-235262/24.
DR   N-PSDB; AAS01431.
XX
PT   Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT   Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT   Wheat Germ Lectin Flashplate assays.
XX
PS   Claim 28; Page 149-153; 160pp; English.
XX
CC   The present sequence represents human secreted calcium channel
CC   alpha2delta subunit #16 which is soluble and retains the functional
CC   characteristics of the full length or wild type alpha2delta subunit
CC   (AAU01025) from which it is derived. The invention relates to truncated
CC   alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC   which retain their affinity for radioactively labelled gabapentin. The
CC   alpha2delta subunit is 1 of the components of the heteromultimeric
CC   voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC   and non-neuronal tissues including heart and skeletal muscle. Numerous
CC   soluble forms of the human calcium channel alpha2delta subunits (AAU01014
CC   -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
CC   calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
CC   The secreted soluble alpha2delta subunit may be used in assays e.g.
CC   scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC   filter binding or wheat germ lectin flashplate assays to detect or
CC   measure the binding or interaction of a ligand (e.g. gabapentin, L-
CC   Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
CC   Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
CC   subunit
XX
SQ   Sequence 1050 AA;

  Query Match             90.4%;  Score 5179;  DB 4;  Length 1050;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches  989;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 777

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 837

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        838 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 897

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 957

Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 1017

Qy        971 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPV 1003
              |||||||||||||||||||||||||||||||||
Db       1018 PCQKVFVVQQIPNSNLLLLVTDPTCDCSIFPPV 1050
```

```
RESULT 13
AAB62260
ID   AAB62260 standard; protein; 1050 AA.
XX
AC   AAB62260;
XX
DT   11-JUN-2001  (first entry)
XX
DE   Human calcium channel alpha2delta subunit.
XX
KW   Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW   nervous system disorder; pain; epilepsy; anxiety; human.
XX
OS   Homo sapiens.
XX
PN   WO200120336-A2.
XX
PD   22-MAR-2001.
XX
PF   18-SEP-2000; 2000WO-EP009136.
XX
PR   16-SEP-1999;   99US-00397549.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Bertelli F,  Brown JP,  Dissanayake V,  Suman-Chauhan N,  Gee NS;
XX
DR   WPI; 2001-257902/26.
XX
PT   Competitive binding assay for screening ligands which bind a cerebral
PT   cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
PT   the ligands identified are useful for treating disorders of the nervous
PT   system, including pain.
XX
PS   Disclosure; Page 147-150; 158pp; English.
XX
CC   The invention relates to a new method for screening ligands which bind a
CC   cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC   preferably alpha2delta-1 subunit. The method comprises contacting a
CC   secreted soluble recombinant alpha2delta-1 subunit with a ligand of
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CC   interest and a labelled compound which binds the subunit, followed by
CC   measuring the level of binding of the labelled compound to alpha2delta-1
CC   subunit. The method is useful for screening ligands, preferably
CC   biologically active products that modulate a nervous system function,
CC   which bind a cerebral cortical voltage-dependent calcium channel
CC   alpha2delta-1 subunit. The ligands identified by the method are useful
CC   for treating disorders of the nervous system, including pain, epilepsy
CC   and anxiety. The present sequence represents a human calcium channel
CC   alpha2delta subunit
XX
SQ   Sequence 1050 AA;

  Query Match             90.4%;  Score 5179;  DB 4;  Length 1050;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches  989;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
              : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy         71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy        131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy        191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy        251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy        311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy        371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy        431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy        491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy        551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy        611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy        671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 777

Qy        731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 837

Qy        791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        838 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 897

Qy        851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 957

Qy        911 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 970
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 FLLEWSVWGSWYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFVYQPAIREANGIVECG 1017

Qy        971 PCQKVPVVQQIPNSNLLLLVTDPTCDCSIFPPV 1003
              |||||||||||||||||||||||||||||||||
Db       1018 PCQKVPVVQQIPNSNLLLLVTDPTCDCSIFPPV 1050


RESULT 14
AAY92323
ID   AAY92323 standard; protein; 1096 AA.
XX
AC   AAY92323;
XX
DT   10-AUG-2000  (first entry)
XX
DE   Human alpha-2-delta-D polypeptide from splice variant 1.
XX
KW   alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
KW   anticonvulsant; antimigrane; antiparkinsonian; antidepressant;
KW   splice variant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 310
FT                   /note= "encoded by RTT"
XX
PN   WO200020450-A2.
XX
PD   13-APR-2000.
XX
PF   07-OCT-1999;   99WO-US023519.
XX
PR   07-OCT-1998;   98US-0103322P.
PR   30-OCT-1998;   98US-0106473P.
PR   29-DEC-1998;   98US-0114088P.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Johns MA,  Moldover B,  Offord JD;
XX
DR   WPI; 2000-303744/26.
DR   N-PSDB; AAA09278.
XX
PT   New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
PT   proteins, useful in the treatment of epilepsy, migraine, chronic pain,
PT   anxiety, multiple sclerosis or cancer.
XX
PS   Example 3; Page 84; 88pp; English.
XX
CC   The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC   The gene has been mapped to chromosome 12p13.1. This gene and the related
CC   alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC   from abnormal calcium flux by introducing expression vectors containing
CC   the respective gene into mammalian cells. The antisense genes are also
CC   useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC   is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC   Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
CC   related syndromes, migraine, ataxia, vestibular defects, chronic pain,
CC   sleep interference, anxiety, amyotropic lateral sclerosis (ALS), multiple
CC   sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
CC   syndromes, mood, depression or cancer
XX
SQ   Sequence 1096 AA;

  Query Match             81.2%;  Score 4649;  DB 3;  Length 1096;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches  895;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;
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```
Qy          11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
               : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          58 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 117

Qy          71 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         118 RRKVEAVQNLVEAAEEADLNHEFNESLVFDYYNSVLINERDEKGNFVELGAEFLLESNAH 177

Qy         131 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 FSNLPVNTSISSVQLPTNVYNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATG 237

Qy         191 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         238 FFRIYPGIKWTPDENGVITFDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297

Qy         251 TTILDTLGENDFVNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 310
               |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         298 TTILDTLGENDFXNIIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVD 357

Qy         311 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         358 QALREAFQILKQFQEAKQGSLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR 417

Qy         371 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         418 EVSFADRMKWIACNNKGYYTQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDS 477

Qy         431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         478 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGY 537

Qy         491 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         538 AFLNTNNGYILSHPDLRPLYREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 597

Qy         551 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDL 610
               |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         598 LSMDVKVPMDKGKRVLFLTNDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDL 657

Qy         611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         658 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTA 717

Qy         671 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 730
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         718 PMEAYWTALALNMSEESEHVVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFT 777

Qy         731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 790
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         778 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAAGV 837

Qy         791 QMKLEFLQRKFWAATRQCSTVDGPYTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 850
               |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         838 QMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVIDNNGFILISKRSRETGRFLGE 897

Qy         851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 910
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVL 957
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RESULT 15
AAE13285
ID   AAE13285 standard; protein; 1310 AA.
XX
AC   AAE13285;
XX
DT   12-FEB-2002  (first entry)
XX
DE   Human transporters and ion channels (TRICH)-12.
XX
KW   Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis;
KW   diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia;
KW   cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia;
KW   neurological disorder; Alzheimer's disease; cataract; infertility;
KW   Wilson's disease; schizophrenia; Grave's disease; addison's disease;
KW   Huntington's disease; multiple sclerosis; meningitis; hypotensive;
KW   cardiant; nootropic; neuroprotective; neuroleptic; ophthalmological;
KW   antithyroid; anticonvulsant; goitre; antiinflammatory.
XX
OS   Homo sapiens.
XX
PN   WO200177174-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-US011206.
XX
PR   06-APR-2000; 2000US-0195595P.
PR   12-APR-2000; 2000US-0196872P.
PR   20-APR-2000; 2000US-0199020P.
PR   28-APR-2000; 2000US-0200552P.
PR   05-MAY-2000; 2000US-0202348P.
PR   11-MAY-2000; 2000US-0203495P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Reddy R, Thornton M, Borowsky ML, Tang YT, Khan FA, Tribouley CM;
PI   Gandhi AR, Yao MG, Sanjanwala MS, Baughn MR, Nguyen DB, Policky JL;
PI   Yue H, Seilhamer JJ, Walia NK, Lal P, Kearney L, Walsh RT, Lu DAM;
PI   Lu Y, Greene BD, Raumann BE, Patterson C;
XX
DR   WPI; 2002-017448/02.
DR   N-PSDB; AAD22004.
XX
PT   Polypeptides of human transporters and ion channels, useful for
PT   diagnosing, treating or preventing disorders of transport, neurological,
PT   muscle, immunological and cell proliferative disorders.
XX
PS   Claim 1; Page 132-135; 150pp; English.
XX
CC   The invention relates to human transporters and ion channels (TRICH) and
CC   the polynucleotides encoding them. The composition comprising TRICH or
CC   agonist of TRICH is useful for treating a disease or condition associated
CC   with decreased expression of functional TRICH or condition associated
CC   with overexpression of TRICH respectively. The composition comprising Ab
CC   is useful for diagnosing a condition of disease associated with
CC   expression of TRICH in a subject, where the disorders include a transport
CC   disorder such as akinesia, cystic fibrosis, diabetes mellitus,
CC   Parkinson's disease, myasthenia gravis, cardiac disorders associated with
CC   transport e.g. angina, hypertension, myocarditis, neurological disorders
CC   associated with transport e.g. Alzheimer's disease, Wilson's disease,
CC   schizophrenia, cataracts, infertility, hyperglycaemia, Grave's disease,
CC   goitre, addison's disease, Huntington's disease, dementia, multiple
CC   sclerosis, bacterial and viral meningitis. TRICH DNA is useful for
CC   generating a transcript image of a tissue or cell type, which represents
CC   the global pattern of gene expression by a particular tissue or cell type
CC   and for analysing the proteome of a tissue or cell type. TRICH DNA is
CC   used in gene therapy. The present amino acid sequence is human TRICH12
CC   protein
XX
SQ   Sequence 1310 AA;

  Query Match             66.5%;  Score 3808;  DB 5;  Length 1310;
  Best Local Similarity   80.5%;  Pred. No. 0;
  Matches  750;  Conservative    4;  Mismatches   14;  Indels  164;  Gaps    2;

Qy          11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 70
               : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         374 ETVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLELVRKFSEDMENML 433

Qy          71 RRKVEAVQNLVEAAEEADLNHEFNESLV------------------------------ 98
               ||||||||||||||||||||||||||||
Db         434 RRKVEAVQNLVEAAEEADLNHEFNESLVEPGVGVGVGMSVTQSGVGVGVGMSVTQSGVGV 493
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Qy         99 ------------------------------------------------------------ 98

Db        494 GVGMSITLSGVGVGVGMSVRQSGVGVGVGMSVTQSGVGVGVGMSVTQSGVGVGVGMSVRQ 553

Qy         99 ------------------------------------------------------------ 98

Db        554 SGVGVGVGMSVTQSWGVFSAQRAAAGACVDSDGRPAPALSSSHLRRFSSSLSACPGARAA 613

Qy         99 ---------FDYYNSVLINERDEKGNFVELGAEFLLESNAHFSNLPVNTSISSVQLPTNV 149
                       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 SVGLTRPPQFDYYNSVLINERDEKGNFVELGAEFLLESNAHFSNLPVNTSISSVQLPTNV 673

Qy        150 YNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFFRIYPGIKWTPDENGVIT 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 YNKDPDILNGVYMSEALNAVFVENFQRDPTLTWQYFGSATGFFRIYPGIKWTPDENGVIT 733

Qy        210 FDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFVNIIAYN 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        734 FDCRNRGWYIQAATSPKDIVILVDVSGSMKGLRMTIAKHTITTILDTLGENDFINIIAYN 793

Qy        270 DYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQG 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 DYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVGVVDQALREAFQILKQFQEAKQG 853

Qy        330 SLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREVSFADRMKWIACNNKGYY 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 SLCNQAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGREVSFADRMKWIACNNKGYY 913

Qy        390 TQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKLLSSQAQSLTLLTTVAMP 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 TQISTLADTQENVMEYLHVLSRPMVINHDHDIIWTEAYMDSKLLSSQAQSLTLLTTVAMP 973

Qy        450 VFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPL 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 VFSKKNETRSHGILLGVVGSDVALRELMKLAPRYKLGVHGYAFLNTNNGYILSHPDLRPL 1033

Qy        510 YREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLSMDVKVPMDKGKRVLFLT 569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 YREGKKLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLSMDVKVPMDKGKRVLFLT 1093

Qy        570 NDYFFTDISDTPFSLGAVLSRGHGEYILLGNTSVEEGLHDLLHPDLALAGDWIYCITDID 629
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1094 NDYFFTDISDTPFSLGVVLSRGHGEYILLGNTSVEEGLHDLLHPDLALAGDWIYCITDID 1153

Qy        630 PDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAPMEAYWTALALNMSEESEH 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1154 PDHRKLSQLEAMIRFLTRKDPDLECDEELVREVLFDAVVTAPMEAYWTALALNMSEESEH 1213

Qy        690 VVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAGSF 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1214 VVDMAFLGTRAGLLRSSLFVGSEKVSDRKFLTPEDEASVFTLDRFPLWYRQASEHPAGSF 1273

Qy        750 VFNLRWAEGPESAGEPMVVTASTAVAVTVDKR 781
              ||||||||||   | |        :  |: ||
Db       1274 VFNLRWAEGP---GRPSAKGLPPPLCQTILKR 1302
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Search completed: November 16, 2005, 03:19:36
Job time : 177 secs